



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 168123**

**TO: Elizabeth McElwain**  
**Location: 2a11 / 2c18**  
**Tuesday, October 11, 2005**  
**Art Unit: 1638**  
**Phone: 571-272-0802**  
**Serial Number: 10 / 060793**

**From: Jan Delaval**  
**Location: Biotech-Chem Library**  
**Remsen 1a51**  
**Phone: 571-272-2504**

**jan.delaval@uspto.gov**

### **Search Notes**

**This Page Blank (uspto)**

STIC-Biotech/ChemLib

168123

From: McElwain, Elizabeth  
Sent: Thursday, October 06, 2005 5:08 PM  
To: STIC-Biotech/ChemLib  
Subject: sequence search

Please search 10/060,793 for SEQ ID NO: 25 and for DNA encoding SEQ ID NO: 26.

Thank you,  
Beth

Elizabeth F. McElwain, Ph.D.  
U.S. Patent and Trademark Office  
Tech Center 1600, Art Unit 1638  
room Remsen 2A11  
mailbox Remsen 2C18  
571-272-0802  
elizabeth.mcelwain@uspto.gov

RECEIVED  
OCT - 7 2005  
STIC-BIOTECH/CHEM. DIVISION  
(STIC)

\*\*\*\*\*  
Searcher: Jan  
Searcher Phone: 22504  
Date Searcher Picked up: 10/14/05  
Date completed: 10/14/05  
Searcher Prep Time: 10  
Online Time: 10

\*\*\*\*\*  
Type of Search  
NA# ✓ AA#:         
S/L:        Oligomer:         
Encode/Transl: ✓  
Structure #:        Text:         
Inventor:        Litigation:       

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Vendors and cost where applicable  
STN:         
DIALOG:         
QUESTEL/ORBIT:         
LEXIS/NEXIS:         
SEQUENCE SYSTEM: ✓  
WWW/Internet:         
Other (Specify):

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 09:50:59 ; Search time 899 Seconds  
(without alignments)  
8343.865 Million cell updates/sec

Title: US-10-060-793A-25  
Perfect score: 1077  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16886260

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:\*

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25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1077	100.0	1077	16	US-10-060-793-25
2	1077	100.0	1077	19	US-10-776-311-41
3	1077	100.0	1077	20	US-10-840-478-3
4	1077	100.0	1077	21	US-10-840-325-35
5	1077	100.0	1077	22	US-10-840-579-5
6	1077	100.0	12456	22	US-10-985-109-95
c 7	1077	100.0	12456	22	US-10-985-254-95

Query Match 100.0%; Score 1077; DB 16; Length 1077;

Best Local Similarity 100.0%; Pred. No. 4.2e-295; Mismatches 0; Indels 0; Gaps 0;

Matches 1077; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGACTGAGGATAAGACGAGGTCCGAGTTCGCCGAGCTCAGGAGCTCAAGCACTCGATC 60

ALIGNMENTS

RESULT 1

US-10-060-793-25

; Sequence 25, Application US/10060793

; Publication No. US20030196217A1

; GENERAL INFORMATION:

; APPLICANT: Abbott Laboratories

; APPLICANT: Mukerji, Pradip

; APPLICANT: Huang, Yung-Sheng

; APPLICANT: Pereira, Suzette L.

; TITLE OF INVENTION: DESATURASE GENES, ENZYMES ENCODED

; TITLE OF INVENTION: THEREBY, AND USES THEREOF

; FILE REFERENCE: 6884.US.O1

; CURRENT APPLICATION NUMBER: US/10/060,793

; CURRENT FILING DATE: 2002-06-24

; NUMBER OF SEQ ID NOS: 60

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 25

; LENGTH: 1077

; TYPE: DNA

; ORGANISM: Saprolegnia diclina

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9 872.2 81.0 1077 21 US-10-840-325-46 Sequence 46, Appl

10 872.2 81.0 1077 22 US-10-840-579-9 Sequence 9, Appl

11 869.6 80.7 10328 21 US-10-840-325-129 Sequence 129, App

12 869.6 80.7 10328 22 US-10-840-579-101 Sequence 101, App

13 158.6 14.7 1263 23 US-11-021-712-29 Sequence 29, Appl

14 113.2 10.5 1543 20 US-10-604-708-10 Sequence 10, Appl

15 113 10.5 1317 19 US-10-437-963-68012 Sequence 68012, A

16 111.2 10.3 1955 20 US-10-425-115-126240 Sequence 126240, A

17 108.4 10.1 1553 20 US-10-425-115-81874 Sequence 81874, A

18 108.2 10.0 1766 20 US-10-739-930-2687 Sequence 2687, Ap

19 107 9.9 1182 16 US-10-060-793-41 Sequence 41, Appl

20 103.8 9.6 1976 19 US-10-437-963-25531 Sequence 25531, A

21 102.2 9.5 1242 20 US-10-437-963-733-7 Sequence 7, Appl

22 101.6 9.4 1797 18 US-10-425-114-19248 Sequence 19248, A

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24 101.6 9.4 1804 20 US-10-604-708-9 Sequence 9, Appl

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27 99.4 9.2 1666 20 US-10-425-115-126274 Sequence 126274, A

28 97.6 9.1 1080 17 US-10-369-493-26432 Sequence 26432, A

29 97.6 9.1 2001 17 US-10-310-154-101 Sequence 101, App

30 97.6 9.1 2001 21 US-10-732-923-186 Sequence 186, App

31 96.6 9.0 103 20 US-10-840-478-76 Sequence 76, Appl

32 96.6 9.0 103 21 US-10-840-325-61 Sequence 61, Appl

33 96.6 9.0 103 22 US-10-840-579-23 Sequence 23, Appl

34 96.6 9.0 104 20 US-10-840-478-75 Sequence 75, Appl

35 96.6 9.0 104 21 US-10-840-325-60 Sequence 60, Appl

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41 91.6 8.5 1724 18 US-10-425-114-25066 Sequence 25066, A

42 91.6 8.5 1729 18 US-10-425-114-21414 Sequence 21414, A

43 91.6 8.5 1729 20 US-10-604-708-8 Sequence 8, Appl

44 91.6 8.5 1739 18 US-10-425-114-30705 Sequence 30705, A

45 91.6 8.5 1743 18 US-10-425-114-31268 Sequence 31268, A

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RESULT 2

US-10-776-311-41

; Sequence 41, Application US/10776311

; Publication No. US20040172682A1

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; GENERAL INFORMATION:
; APPLICANT: Edgar B. Cahoon
; APPLICANT: Howard G. Damude
; APPLICANT: William D. Hitz
; APPLICANT: Anthony J. Kinney
; APPLICANT: Charles W. Kolar
; APPLICANT: Zhan Bin Liu
; TITLE OF INVENTION: Production of Long Chain Polyunsaturated Fatty Acids in Plants
; FILE REFERENCE: B01538 US NA
; CURRENT APPLICATION NUMBER: US/10/776,311
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: US 60/446,941
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 41
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Saprolegnia diclina
US-10-776-311-41
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Best Local Similarity 100.0%; Pred. No. 4,2e-295;
Matches 1077; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Publication No. US2004025321A1  
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; APPLICANT: E.I. du Pont de Nemours and Company, Inc.  
; APPLICANT: Zhu, Quinn  
; APPLICANT: Picataggio, Stephen K.  
; TITLE OF INVENTION: OPTIMIZED GENES FOR THE PRODUCTION OF OMEGA FATTY ACIDS IN  
; TITLE OF INVENTION: OLEAGINOUS YEASTS  
; FILE REFERENCE: CL2234 US NA  
; CURRENT APPLICATION NUMBER: US/10/840,478  
; CURRENT FILING DATE: 2004-05-06  
; PRIOR APPLICATION NUMBER: US60/468718  
; PRIOR FILING DATE: 2003-05-07  
; PRIOR APPLICATION NUMBER: US60/468677  
; PRIOR FILING DATE: 2003-05-07  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 1077  
; TYPE: DNA  
; ORGANISM: Saprolegnia diclina (ATCC #56851)  
US-10-840-478-3

Query Match 100.0%; Score 1077; DB 20; Length 1077;  
Best Local Similarity 100.0%; Pred. No. 4.2e-295;  
Matches 1077; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGACTGAGGATAGACGAAGTGGTTCGGAGCTCAGGAGCTCAAGCACTCGATC 60  
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301 AGCGTCAACTTTATCATCGCTGCATCATGCATCTCTCGGATTTTGACGCCGTTGAGAGC 360  
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361 TGGCGGTGACGACCGCCACCAACCAAGAACACGGGCAACATTGATAGGACGAGATC 420  
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RESULT 4  
US-10-840-325-35  
; Sequence 35, Application US/10840325  
; Publication No. US20050043527A1  
; GENERAL INFORMATION:  
; APPLICANT: E.I. du Pont de Nemours and Company, Inc.  
; APPLICANT: Yadava, Narendra  
; TITLE OF INVENTION: A DELTA-12 DESATURASE GENE SUITABLE FOR ALTERING LEVELS OF  
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN OLEAGINOUS YEASTS  
; FILE REFERENCE: CL2301  
; CURRENT APPLICATION NUMBER: US/10/840,325  
; CURRENT FILING DATE: 2004-05-06  
; PRIOR APPLICATION NUMBER: US 60/484209  
; PRIOR FILING DATE: 2003-06-30  
; PRIOR APPLICATION NUMBER: US 60/468677  
; PRIOR FILING DATE: 2003-05-07  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 35

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; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Saprolegnia diclina
US-10-840-325-35

Query Match      100.0%; Score 1077; DB 21; Length 1077;
Best Local Similarity 100.0%; Pred. No. 4.2e-295;
Matches 1077; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGACTGAGGATAAGACGAAGGTCGAGTTCGCCAGCGCTACGGAGCTCAAGCACTCGATC 60
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DB 61 CCGAACCGGTGCTTTGAGTTCGAACCTCGGCTCTCGCTCTACTACACGGCCGCGCATC 120
QY 121 TTCAACCGGTGCGGCTCGGCGGCGTCTCTACGCGCGCGCTCGACGCGCTTCATTGCC 180
DB 121 TTCAACCGGTGCGGCTCGGCGGCGTCTCTACGCGCGCGCTCGACGCGCTTCATTGCC 180
QY 181 GATAACGTTCTGCTCCAGCGGCTGCTTTGCGCCACCTACATCTACGTGAGGGGCGTCATC 240
DB 181 GATAACGTTCTGCTCCAGCGGCTGCTTTGCGCCACCTACATCTACGTGAGGGGCGTCATC 240
QY 241 TTCTGGGGCTTCTTCACGCGTCGGCCACGACTGCGGCCACTCGGCTTCTCGCGCTACCAC 300
DB 241 TTCTGGGGCTTCTTCACGCGTCGGCCACGACTGCGGCCACTCGGCTTCTCGCGCTACCAC 300
QY 301 AGCGTCAACTTTATCATCGGCTGCGATCATGCACTCTCGGATTTTGACGCGCTTCGAGAGC 360
DB 301 AGCGTCAACTTTATCATCGGCTGCGATCATGCACTCTCGGATTTTGACGCGCTTCGAGAGC 360
QY 361 TGGCGGTGAGCAACCGCCACCAACCAAGAACACGCGGCAACATTGATAAGGACGAGATC 420
DB 361 TGGCGGTGAGCAACCGCCACCAACCAAGAACACGCGGCAACATTGATAAGGACGAGATC 420
QY 421 TTTTACCGGACACCGGTGCGTCAAGGACTCTCAGGAGCTCGGCGCTCATCGTCTACACGCTC 480
DB 421 TTTTACCGGACACCGGTGCGTCAAGGACTCTCAGGAGCTCGGCGCTCATCGTCTACACGCTC 480
QY 481 GCGGTGCGTGGTGTCTTCTAAGGTCGAGTTCGCGGCGCTCGACGCGCTTCATTGCC 180
DB 481 GCGGTGCGTGGTGTCTTCTAAGGTCGAGTTCGCGGCGCTCGACGCGCTTCATTGCC 180
QY 541 GACCCGTGGGACCGGCTCCTTCGCGCGCGCTCGGCGCTCATCGTCTCGCGGTC 600
DB 541 GACCCGTGGGACCGGCTCCTTCGCGCGCGCTCGGCGCTCATCGTCTCGCGGTC 600

RESULT 5
US-10-840-579-5
; Sequence 5, Application US/10840579
; Publication No. US20050136519A1
; GENERAL INFORMATION:
; APPLICANT: E.I. du Pont de Nemours and Company, Inc.
; TITLE OF INVENTION: PRODUCTION OF OMEGA FATTY ACIDS IN OLEAGINOUS YEASTS
; FILE REFERENCE: CL2233 PCT
; CURRENT APPLICATION NUMBER: US/10/840,579
; CURRENT FILING DATE: 2004-05-06
; PRIOR APPLICATION NUMBER: US 60/468677
; PRIOR FILING DATE: 2003-05-07
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Saprolegnia diclina (ATCC #56851)
US-10-840-579-5

Query Match      100.0%; Score 1077; DB 22; Length 1077;
Best Local Similarity 100.0%; Pred. No. 4.2e-295;
Matches 1077; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACTGAGGATAAGACGAAGTTCGAGTTCGCCAGCGCTACGGAGCTCAAGCACTCGATC 60
DB 1 ATGACTGAGGATAAGACGAAGTTCGAGTTCGCCAGCGCTACGGAGCTCAAGCACTCGATC 60
QY 61 CCGAACCGGTGCTTTGAGTTCGAACCTCGGCTCTCGCTCTACTACACGGCCGCGCATC 120
DB 61 CCGAACCGGTGCTTTGAGTTCGAACCTCGGCTCTCGCTCTACTACACGGCCGCGCATC 120
QY 121 TTCAACCGGTGCGGCTCGGCGGCGTCTCTACGCGCGCGCTCGACGCGCTTCATTGCC 180
DB 121 TTCAACCGGTGCGGCTCGGCGGCGTCTCTACGCGCGCGCTCGACGCGCTTCATTGCC 180
QY 181 GATAACGTTCTGCTCCAGCGGCTGCTTTGCGCCACCTACATCTACGTGAGGGGCGTCATC 240
DB 181 GATAACGTTCTGCTCCAGCGGCTGCTTTGCGCCACCTACATCTACGTGAGGGGCGTCATC 240
QY 241 TTCTGGGGCTTCTTCACGCGTCGGCCACGACTGCGGCCACTCGGCTTCTCGCGCTACCAC 300
DB 241 TTCTGGGGCTTCTTCACGCGTCGGCCACGACTGCGGCCACTCGGCTTCTCGCGCTACCAC 300
QY 301 AGCGTCAACTTTATCATCGGCTGCGATCATGCACTCTCGGATTTTGACGCGCTTCGAGAGC 360
DB 301 AGCGTCAACTTTATCATCGGCTGCGATCATGCACTCTCGGATTTTGACGCGCTTCGAGAGC 360
QY 361 TGGCGGTGAGCAACCGCCACCAACCAAGAACACGCGGCAACATTGATAAGGACGAGATC 420
DB 361 TGGCGGTGAGCAACCGCCACCAACCAAGAACACGCGGCAACATTGATAAGGACGAGATC 420
QY 421 TTTTACCGGACACCGGTGCGTCAAGGACTCTCAGGAGCTCGGCGCTCATCGTCTACACGCTC 480
DB 421 TTTTACCGGACACCGGTGCGTCAAGGACTCTCAGGAGCTCGGCGCTCATCGTCTACACGCTC 480
QY 481 GCGGTGCGTGGTGTCTTCTAAGGTCGAGTTCGCGGCGCTCGACGCGCTTCATTGCC 180
DB 481 GCGGTGCGTGGTGTCTTCTAAGGTCGAGTTCGCGGCGCTCGACGCGCTTCATTGCC 180
QY 541 GACCCGTGGGACCGGCTCCTTCGCGCGCGCTCGGCGCTCATCGTCTCGCGGTC 600
DB 541 GACCCGTGGGACCGGCTCCTTCGCGCGCGCTCGGCGCTCATCGTCTCGCGGTC 600
```



; TITLE OF INVENTION: DELTA 15 DESATURASES SUITABLE FOR ALTERING LEVELS OF  
; FILE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN OLEAGINOUS YEAST  
; CURRENT APPLICATION NUMBER: US/10/985,254  
; CURRENT FILING DATE: 2004-11-10  
; PRIOR APPLICATION NUMBER: US 60/519191  
; PRIOR FILING DATE: 2003-11-12  
; NUMBER OF SEQ ID NOS: 109  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 95  
; LENGTH: 12456  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: plasmid pKF585  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1201)..(1201)  
; OTHER INFORMATION: n is a, c, g, or t  
US-10-985-254-95

Query Match 100.0%; Score 1077; DB 22; Length 12456;  
Best Local Similarity 100.0%; Pred. No. 6.8e-295;  
Matches 1077; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGACTGAGGATAAGACGAAGGTCGAGTTCCTCCGACGCTCACGGAGCTCAAGCACTCGATC 60
DB 10446 ATGACTGAGGATAGACGAAGGTCGAGTTCCTCCGACGCTCACGGAGCTCAAGCACTCGATC 10387

QY 61 CCGAACCGTGTCTTGGTGTGAGTCTGAGTCTCGGCTCTCTGCTCTACTACAGCGCCGCGGATC 120
DB 10386 CCGAACCGTGTCTTGGTGTGAGTCTGAGTCTGAGTCTCTGCTCTACTACAGCGCCGCGGATC 10327

QY 121 TTCAACCGTGTGCTTCCGCGGCTCGGCTCTCTAGCGCGGCTCTGAGCGCGCTTCATTTGCC 180
DB 10326 TTCAACCGTGTGCTTCCGCGGCTCGGCTCTCTAGCGCGGCTCTGAGCGCGCTTCATTTGCC 10267

QY 181 GATAACGTTCTGCTTCCACGGCTCGTGTTCGCGCACTTACATCTACGTGACGGCGTTCATC 240
DB 10266 GATAACGTTCTGCTTCCACGGCTCGTGTTCGCGCACTTACATCTACGTGACGGCGTTCATC 10207

QY 241 TTCTGGGGCTTCTTTCACGGTCTGCGCCACGACTGCGGCGCTCTCGGCTCTCTCGGCTACCC 300
DB 10206 TTCTGGGGCTTCTTTCACGGTCTGCGCCACGACTGCGGCGCTCTCGGCTCTCTCGGCTACCC 10147

QY 301 AGCGTCAACTTTATCATCGCTGCTGATCATGCTCTGCGATTTTACGCGCTTCGAGAGC 360
DB 10146 AGCGTCAACTTTATCATCGCTGCTGATCATGCTCTGCGATTTTACGCGCTTCGAGAGC 10087

QY 361 TGGCGGCTGACGCAACCGCCACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGC 420
DB 10086 TGGCGGCTGACGCAACCGCCACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGC 10027

QY 421 TTTTACCCGACCGGTCGGTCAAGGACCTCAGGACCTCAGGACCTCAGGACCTCAGGACCTCAG 480
DB 10026 TTTTACCCGACCGGTCGGTCAAGGACCTCAGGACCTCAGGACCTCAGGACCTCAGGACCTCAG 9967

QY 481 GCGGTCGGTGGTGTGCTTACTTGAAGGTTCGGGTATGCCCGCGCGACGATGAGCCATT 540
DB 9966 GCGGTCGGTGGTGTGCTTACTTGAAGGTTCGGGTATGCCCGCGCGACGATGAGCCATT 9907

QY 541 GACCCGTGGACCGGCTCTCTTTCGCGCGGCTCGGCGGCTCATGTCGCTCGGCGTC 600
DB 9906 GACCCGTGGACCGGCTCTCTTTCGCGCGGCTCGGCGGCTCATGTCGCTCGGCGTC 9847

QY 601 TGGGCGGCTTCTTTCGCGCGGCTACGCGTACCTCACAFACTCGCTCGGCTTTTGGCGTCATG 660
DB 9846 TGGGCGGCTTCTTTCGCGCGGCTACGCGTACCTCACAFACTCGCTCGGCTTTTGGCGTCATG 9787

QY 661 GGCTCTACTACTATGCGCGGCTTTTGTCTTTGCTTCTGCTTCTGCTCATATGACCTTC 720
DB 9786 GGCTCTACTACTATGCGCGGCTTTTGTCTTTGCTTCTGCTTCTGCTCATATGACCTTC 9727
```

## RESULT 8

US-10-840-478-62  
; Sequence 62, Application US/10840478  
; Publication No. US20040253621A1  
; GENERAL INFORMATION:  
; APPLICANT: E.I. du Pont de Nemours and Company, Inc.  
; APPLICANT: Zhu, Quinn  
; APPLICANT: Picataggio, Stephen K.  
; TITLE OF INVENTION: OPTIMIZED GENES FOR THE PRODUCTION OF OMEGA FATTY ACIDS IN  
; FILE OF INVENTION: OLEAGINOUS YEASTS  
; FILE REFERENCE: CL2234 US NA  
; CURRENT APPLICATION NUMBER: US/10/840,478  
; CURRENT FILING DATE: 2004-05-06  
; PRIOR APPLICATION NUMBER: US60/468718  
; PRIOR FILING DATE: 2003-05-07  
; PRIOR APPLICATION NUMBER: US60/468677  
; PRIOR FILING DATE: 2003-05-07  
; NUMBER OF SEQ ID NOS: 122  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 62  
; LENGTH: 1077  
; TYPE: DNA  
; ORGANISM: Saprolegnia diclina  
US-10-840-478-62

Query Match 81.0%; Score 872.2; DB 20; Length 1077;  
Best Local Similarity 88.1%; Pred. No. 5.1e-237;  
Matches 949; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

```
QY 1 ATGACTGAGGATAAGACGAAGGTCGAGTTCCTCCGACGCTCACGGAGCTCAAGCACTCGATC 60
DB 1 ATGGCTGAGGATAAGACGAAGGTCGAGTTCCTTACCTGACTGAGCTGAAGCACTCTATC 60

QY 61 CCGAACCGGTCGCTTTGAGTTCGAACCTTCGCGCTCTCGGCTCTCTGCTCTACTACAGCGCCGCGGATC 120
DB 61 CTTAACCGGTCGCTTTGAGTTCGAACCTTCGAGTCTCGGCTCTCTGCTCTACTACAGCTGCGCGGATC 120

QY 121 TTCAACCGGTCGCGCTTCGGCGGCTGCTCTACGCGCGGCTTCGACGCGGCTTCATTGCC 180
DB 121 TTCAACCGCATCTGCCCTTCTGCTCTGCTCTAGCTGCGCGATCTACTTCCCTTCATTGCC 180

QY 181 GATAACGCTTCTGCTCCACGCGCTCTGTTTGGCGCACCTACATCTACGTGACGGCGTCAATC 240
DB 181 GATAACGCTTCTGCTCCACGCGCTCTGTTTGGCGCACCTACATCTACGTGACGGGTGTTCATC 240

QY 241 TTCTGGGGCTTCTTTCACGGTTCGCGCACGACTGCGGCGCTTCGCGCTTCTCGCGCTACCCAC 300
DB 241 TTCTGGGGCTTCTTTCACGGTTCGCGCACGACTGCGGCGCTTCGCGCTTCTCGCGATACCCAC 300
```





Qy 961 ATACGCGCTTCTTCAAGACGCGGCACCTCTTTGTCAACTACGCGCTGTGCCGAGACG 1020  
Db |||  
961 ATTAAGCTCTTCTTCAAGACGCGTCACTCTTTGTCAACTACGAGCTGTGCCGAGACT 1020  
Qy 1021 GCGCAGATCTTCAGCTCAAGAGTCCGCGCGCGCCGCAAGGCAAGTCCGACTAA 1077  
Db |||  
1021 GCTCAGATTTTCAACCTCAAGAGTCTGCGCGCTGACGCCAAGGCCAAGAGCGACTAA 1077

RESULT 10  
US-10-840-579-9  
; Sequence 9, Application US/10840579  
; Publication No. US20050136519A1  
; GENERAL INFORMATION:  
; APPLICANT: E.I. du Pont de Nemours and Company, Inc.  
; TITLE OF INVENTION: PRODUCTION OF OMEGA FATTY ACIDS IN OLEAGINOUS YEASTS  
; FILE REFERENCE: CL2233 PCT  
; CURRENT APPLICATION NUMBER: US/10/840,579  
; PRIOR FILING DATE: 2004-05-06  
; PRIOR APPLICATION NUMBER: US 60/468677  
; PRIOR FILING DATE: 2003-05-07  
; NUMBER OF SEQ ID NOS: 126  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 1077  
; TYPE: DNA  
; ORGANISM: Saprolegnia declina  
US-10-840-579-9

Query Match 81.0%; Score 872.2; DB 22; Length 1077;  
Best Local Similarity 88.1%; Pred. No. 5.1e-237;  
Matches 949; Conservative 0; Mismatches 128; Indels 0; Gaps 0;

Qy 1 ATGACTGAGGATAGACGAGGTGAGTCCCGAGGCTACGAGCTCAAGCACTCGATC 60  
Db |||  
1 ATGCTGAGGATAAGACCAAGGTGAGTCCCTACCTGACTGAGTGAAGCACTCTATC 60  
Qy 61 CCGAACCGTCTTGTAGTTCGAACCTCGGCTCTCTGCTCTACTACACGCGCGCGCATC 120  
Db |||  
61 CCTAACGCTTGTGTAGTTCGAACCTCGGACTCTGCTCTACTACACTGCGCGAGCATC 120  
Qy 121 TTCAACCGTCTGCGGCGCTGCTCTACGCGCGCGCTGACGCGCGTTCATGTC 180  
Db |||  
121 TTCAACGATCTGCTCTGCTCTGCTCTGCTCTACGCTGCCGATCTACTCGCTTCAITGCC 180  
Qy 181 GATAACGTTCTGCTCCACGCGCTGTTTGGCCACCTACATCTACGTGAGGGCGTCATC 240  
Db |||  
181 GATAACGTTCTGCTCCACGCTCTGTTTGGCCACCTACATCTACGTGAGGGGTGTCATC 240  
Qy 241 TTCTGGGGCTTCTTCAAGGTCGGCCACGACTCGCGCCACTCGGCTTCTCGCGTACCAC 300  
Db |||  
241 TTCTGGGGTCTTCTTACCGTCCGTACGACTGTGCTCCTCTGCTTCTCCGATACCAC 300  
Qy 301 AGCTCAACTTTATCATCGGTGATCATGCACTCTCGCATTTTGACGCGCTTCGAGAGC 360  
Db |||  
301 TCCGTCAACTTATCATTTGGTGTGATCATGCACTCTGCCATCTGACTTCCGCTTCGAGTCC 360  
Qy 361 TGGCGCTGACGACCGCCACCCACCAAGAACAGCGGGCAACATTGTATAGGACGATC 420  
Db |||  
361 TGGCGAGTGACCCACCCACCACTCAAGAACACTGGCAACATTGTATAGGACGAGATC 420  
Qy 421 TTTTACCGCACCGGTTCGCTCAAGGACTCTCAGGACGTGGCCAAATGGGTCTACACGCTC 480  
Db |||  
421 TTCTACCTCATCGTCCGTCAAGGACTCTCAGGACGTGGCAATGGGTCTACACCTC 480  
Qy 481 GCGGGTGGTGGTGTGCTTGAAGGTGGGTATGCGCCGCGCACGATGAGCCATTT 540  
Db |||  
481 GGAGGTGCTGGTGTGCTTGAAGGTGGGTATGCTCTCTCGAACCATGTCCCACTTT 540  
Qy 541 GACCGGTGGACCGCTCTCTTTCGCGCGCGCTGCGCGCTCATCGTGTGCTCGGCGTC 600  
Db |||  
541 GACCCCTGGGACCTCTCTCTTCGACGAGCCTCCGCTGTCTGCTGCTCGGAGTC 600

Qy 601 TGGGCGCGCTTCTTCCGCGGTACGCGTACCTCACATACCTCGCTCGCTTTGCGGTCAAG 660  
Db |||  
601 TGGGCTGCGCTTCTTCCGCTGCGTACGCTACCTCACATACCTCGCTCGCTTTGCGGTCAAG 660  
Qy 661 GGCTCTACTACTATAGCGCGCTTCTTGTCTTGTCTTGTCTCTGCTCATAGACCTTC 720  
Db |||  
661 GGCTCTACTACTATAGCTCTCTTGTCTTGTCTTGTCTCTGCTCATTAACCTTC 720  
Qy 721 TTGCACCAACGACGACGCGCTGTACGCGGCTCGGAGTGGAGTGGAGTACGTCAAG 780  
Db |||  
721 TTGCATCACAAACGACGAGCTACTCTCGTGTAGGTGACTCGGAGTGGAGTACGTCAAG 780  
Qy 781 GGCAACCTCTCGAGCGTTCGACCGCTCGTACGCGCGTTCGTGACAACTCTGAGCCACCAC 840  
Db |||  
781 GGCAACCTGAGCTCCGTCGACCGATCGTACGAGCTTTCGTGACAACTGTCTCACCCAC 840  
Qy 841 ATTGGCAGCAGCAGGTTCACCACTTGTTCCTCGATCATTCGCGCACTACAAGCTCAACGAA 900  
Db |||  
841 ATTGGCAGCAGCAGGTTCATCACTTGTTCCTCATCATTCCTCCCACTACAAGCTCAACGAA 900  
Qy 901 GCCACCAAGCACTTTCGCGCGGTACCCGCACTCGTGCGCAGGAAACGACGAGCCCATC 960  
Db |||  
901 GCCACCAAGCACTTTCGCGCGTTCACCTCCTGAGAGCTAACGACGAGCCCATC 960  
Qy 961 ATCAGCGCTTCTTCAAGACCGCGCACCTCTTTGTCAACTACGCGCTGTGCCGAGACG 1020  
Db |||  
961 ATTACTGCGCTTCTTCAAGACCGCTCACCTCTTTGTCAACTACGAGCTGTGCCGAGACT 1020  
Qy 1021 GCGCAGATCTTCAAGCTCAAGAGTTCGCGCGCGCGCCGAGCCAAAGTCCGACTAA 1077  
Db |||  
1021 GCTCAGATTTTCAACCTCAAGAGTCTGCGGCTGACGCCAAGGCCAAGAGCGACTAA 1077

## RESULT 11

US-10-840-325-129  
; Sequence 129, Application US/10840325  
; Publication No. US20050043527A1  
; GENERAL INFORMATION:  
; APPLICANT: E.I. du Pont de Nemours and Company, Inc.  
; APPLICANT: Yadav, Narendra  
; TITLE OF INVENTION: A DELTA-12 DESATURASE GENE SUITABLE FOR ALTERING LEVELS OF  
; TITLE OF INVENTION: POLYUNSATURATED FATTY ACIDS IN OLEAGINOUS YEASTS  
; FILE REFERENCE: CL2301  
; CURRENT APPLICATION NUMBER: US/10/840,325  
; CURRENT FILING DATE: 2004-05-06  
; PRIOR APPLICATION NUMBER: US 60/484209  
; PRIOR FILING DATE: 2003-06-30  
; PRIOR APPLICATION NUMBER: US 60/468677  
; PRIOR FILING DATE: 2003-05-07  
; NUMBER OF SEQ ID NOS: 130  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 129  
; LENGTH: 10328  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: 10328 bp fragment for integration and expression of the delta-6,  
; OTHER INFORMATION: delta-5, and delta-17 desaturase genes and the elongase gene  
US-10-840-325-129

Query Match 80.7%; Score 869.6; DB 21; Length 10328;  
Best Local Similarity 88.0%; Pred. No. 4.3e-236;  
Matches 947; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

Qy 1 ATGACTGAGGATAAGACGAGTTCGAGTTCCTCCGACGCTACGAGCTCAAGCACTCGATC 60  
Db |||  
6476 ATGCTGAGGATAAGACCAAGGTTCGAGTTCCTTCCCTGACTGAGCTGAAGCACTCTATC 6535  
Qy 61 CCGAACGCGTCTTTCGAGTTCGAACCTTCGCTCTCTACTACACGCGCGCGCATC 120  
Db |||  
6536 CCTAACGCTTGTCTTTCGAGTTCGAACCTTCGAGTTCGCTCTCTACTACACTGCGCGAGCATC 6595  
Qy 121 TTCAACGCGTTCGCGCTTCGCGCGCGCTGCTCTACGCGCGCGCTCGAGCGCTTCAATTGCC 180





Qy 841 ATTGGCAGCAGGTCACCACTTGTTCGGATCATTCGCACTACAAGCTCAACGAA 900  
|||||  
Db 7316 ATTGGCAGCAGGTCACCACTTGTTCGGATCATTCGCACTACAAGCTCAACGAA 7375  
|||||  
Qy 901 GCCACCAAGCACTTTGCGGCGCGTACCGGACCTCGTGCGCAGAAAGCAGAGCCCATC 960  
|||||  
Db 7376 GCCACCAAGCACTTTGCGGCGCTTACCCCTCACCTCGTGAGACGTAACGAGGAGCCCATC 7435  
|||||  
Qy 961 ATCAGGCGCTTCTCAAGACGCGGACCTCTTTGTCAACTACGGCGCTGTGCCGAGAGC 1020  
|||||  
Db 7436 ATTAAGCGCTTCTCAAGACGCGCTCACCTCTTTGTCAACTACGGAGCTGTGCCGAGACT 7495  
|||||  
Qy 1021 GCGCAGATCTTTCAGCTCAAGAGTTCGCGCGCGCGCCCAAGGCCAAAGTCGGACTA 1076  
|||||  
Db 7496 GCTCAGATTTTCACCTCAAGAGTCTGCGCTGCAGCCCAAGGCCAAAGGAGGACCA 7551  
|||||

RESULT 13  
US-11-021-712-29  
; Sequence 29, Application US/11021712  
; Publication No. US20050112719A1  
; GENERAL INFORMATION:  
; APPLICANT: Roesler, Paul  
; APPLICANT: Matthews, T. Dave  
; APPLICANT: Ramseier, Tom  
; APPLICANT: Metz, James  
; TITLE OF INVENTION: Product and Process for Transformation of Thraustochytriales  
; FILE OF INVENTION: Microorganisms  
; FILE REFERENCE: 2997-23  
; CURRENT APPLICATION NUMBER: US/11/021,712  
; PRIOR FILING DATE: 2004-12-23  
; PRIOR APPLICATION NUMBER: US/10/124,807  
; PRIOR FILING DATE: 2002-04-16  
; PRIOR APPLICATION NUMBER: 60/284,116  
; PRIOR FILING DATE: 2001-04-16  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 29  
; LENGTH: 1263  
; TYPE: DNA  
; ORGANISM: Caenorhabditis elegans  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (23)..(1228)  
; OTHER INFORMATION:  
US-11-021-712-29

Query Match 14.7%; Score 158.6; DB 23; Length 1263;  
Best Local Similarity 52.2%; Pred. No. 1.2e-34;  
Matches 434; Conservative 0; Mismatches 380; Indels 18; Gaps 3;  
Qy 203 TCGTTTCGGCACCCTACATCTAGCTGCGAGGCGTCATCTTCTGGGGTCTTTCACGGTGC 262  
|||||  
Db 327 TCGGCTACCTCGTGTGAACATCTTTCATGGGCGCTTTCGGCTTCGCGCTTCTGCTGTCG 386  
|||||  
Qy 263 GCACGACTCGGCGCACTCGGCTTTCGCGCTACACGCTCACTTTATCATCGCT 322  
|||||  
Db 387 GCACGACTCGCTCCACGGAAGCTTTCGGAACACCAAGAACCTTCAAGCTTATCGGCC 446  
|||||  
Qy 323 GCATCATGCACTCTGCGATTTTGACGCGCTTCGAGAGCTGGCGGTGACGCAACCGCCACC 382  
|||||  
Db 447 ACATCGCTTCTGCGCCCTCTTCTGCGCTTCTTCCCTTCGAGAGTTCGACAAAGTCC 506  
|||||  
Qy 383 ACCAAGAGACACGGGCAACATTGATAAGA-----CGAGATCTTTTACCCGACCGGT 436  
|||||  
Db 507 ACCACGCTTTCACCAACCATCATGACAAAGGACCAACGCGCCACGCTTGGATCCAGGACAAG 566  
|||||  
Qy 437 CGGTCAAGGACCTCCAGGAGCTGGCAATGGGTCTACAGCTCGGCGGTGCGTGGTTG 496  
|||||  
Db 567 ACTGGAGGGGCATGCCCTCGTGAAGCGCTGGTTTCAACCCCATCCCTTCTCGGGCTGGC 626  
|||||  
Qy 497 TCTACTTGAAGGTGCGGTATGCCCCGCGCAGATGAGC-----CACTTTGACCCGT 547  
|||||

Db 627 TCAAGTGTTCGCCGTACACACCTCTTCGGCTTCGCGAGCGCTCGCACTTCTGGGCCCT 686  
|||||  
Qy 548 GGGACCGGCTCTCTTCGCGCGCGGTGGCGCGTATCGGTGTCGTCGGCGTCTGGGCCG 607  
|||||  
Db 687 ACTCGTGTCTTCGTCGCGCAACTCGGACCGCGCTCCAGTCCGATCAGCGGATCTGCT 746  
|||||  
Qy 608 CTTTCGCGCGGTACGCGTACCTCACATACCTCGCTCGGCTTTCGGCTATCGGCTCT 667  
|||||  
Db 747 GCTGCGTTCGCGCTACATCGCCCTCACCATCGCGCTCGTACTCGAACTGGTTCGGT 806  
|||||  
Qy 668 ACTACTATGCGCGCTCTTTGTCTTTCGTTTCGTTTCGTTTCATTAAGACCTTCTTGCA 727  
|||||  
Db 807 ACTACTGGTTCGCGCTCTCGTTCTTCGCGCTCATGTCGTCGTCACCTACTCTG 866  
|||||  
Qy 728 ACAACGACGAGGAGCGCGCTGTGACGCGACTCGGAGTGGAGTGTAGTCAAGGGCAACC 787  
|||||  
Db 867 ACGTGACGAGCTGCGCGAGGTCTACGAGGCGGACGAGTGTGTCGTCGCGCGCGAGA 926  
|||||  
Qy 788 TCTCGAGCGTCGACCGCTCGTACGCGCGGTTCGTGGACAACTGAGCCACACAT---TG 844  
|||||  
Db 927 CCAGACCATCGACCGCTACTACGGCTCGGCTCGACACCATGACCATCATACCG 986  
|||||  
Qy 845 GCAAGCAGGCTCCACCACTTGTTCGCGATCATTCGCACTACAAGCTCAACGAAAGCCA 904  
|||||  
Db 987 ACGGCACGTTGGCCCACTTCTTCAACAAGATCCGCACTACCACTTCTCATCGAGGCCA 1046  
|||||  
Qy 905 CCAAGCACTTTGGCGCGCGGTACCGGACCTCTGTCGCGAGGAGGAGGAGCCCATCATCA 964  
|||||  
Db 1047 CCGAGGGCGTCAAGAAAGTCTCTGAGCCCTCTCGGACACCCAGTACGGGTACAAAGTCG 1106  
|||||  
Qy 965 CGGCTTCTTCAAGACGCGGCACTCTTTGTCAACTAGGCGCTGTGCCGGA 1016  
|||||  
Db 1107 AGGTCAACTACGACTTCTTCGCGCGCTTCTCTGTTCAACTACAAGCTCGA 1158  
|||||

RESULT 14  
US-10-604-708-10  
; Sequence 10, Application US/10604708  
; Publication No. US20040221335A1  
; GENERAL INFORMATION:  
; APPLICANT: Shewmaker, Christine K  
; APPLICANT: Van Eenennaam, Allison  
; APPLICANT: Hawkins, Debra T  
; APPLICANT: Sanders, Rick  
; TITLE OF INVENTION: Methods for Increasing Total Oil Levels in Plants  
; FILE REFERENCE: 38-77(52794)  
; CURRENT APPLICATION NUMBER: US/10/604,708  
; CURRENT FILING DATE: 2003-08-12  
; PRIOR APPLICATION NUMBER: US 60/402,527  
; PRIOR FILING DATE: 2002-08-12  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 10  
; LENGTH: 1543  
; TYPE: DNA  
; ORGANISM: Zea mays  
US-10-604-708-10

Query Match 10.5%; Score 113.2; DB 20; Length 1543;  
Best Local Similarity 48.1%; Pred. No. 9.3e-22;  
Matches 478; Conservative 0; Mismatches 453; Indels 63; Gaps 3;  
Qy 34 ACCTCAGGAGCTCAAGACTCGATCCCGAAGCGGTGCTTTAGTCAAGACCTCGGCTC 93  
|||||  
Db 257 ACCTAGCGACCTCAGGAAGGCCATCCCGCGCACTGCTTCAGCGCTCGCTCATCAGG 316  
|||||  
Qy 94 TCGCTCTACTACAGCGCGCGGATCTTCAACGCGTTCGCGCTCGGCGGTGCTCTAC 153  
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Db 317 TCTGTCTTCTTCTCGCCACGACCTCGCCATCG-----CCGCGGGCTCTCTG 367  
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Qy 154 GCGGCGGCTCGAGCGCGGTTCATTGCGGATCAAGCTTCTGCTCCACGCGCTCGTTGCGCC 213  
|||||

Db 368 TTGGCTCTGGCGCTCATCCCGCCTCCCGGGCTCTCTCCGCGCGCGCTGGCG 427  
Qy 214 ACCTACATCTACGTGACGGGGCTCATCTTCTGGGGCTTCTTTCAGCGTGGCCACGACTGC 273  
Db 428 CTCTACTTGGGGCGCGCAGGCGAGCATGATGTTCCGGCTGTGGTGCATCGCGCAGAGTGC 487  
Qy 274 GGCCACTCGGCTTCTCGCGTACACAGCGTCAACTTTATCATCGGCTGCATCATGCAC 333  
Db 488 GGGACAGCAGCTTCTCCCGTACGGCTCTCAACAGCGCTCTGGCTGGTCTGCAC 547  
Qy 334 TCTCGATTTTTCAGCGCTTTCAGAGCTGGCGCTGAGCGTGGACCGCCACCCACCAAGAAC 393  
Db 548 TCGTGCCTCTTCGCGCCCTACTTCTCGTGAAGTACAGCCACCGCGCCACCGCCAAC 607  
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Db 608 ACCCGCTCTTCGGAGCGCGAGAGTGTCTGCGCCCAAGCAGAGCGCCGAGATCCCGTGG 667  
Qy 445 GACCTCCAGGACGTGCGCAATGGTCTACACGCTCGCGGTGCGTGTGTTGTTCTACTTG 504  
Db 668 TACTCCCGCTGTGTACAGCGGCAAAACCCCGTGGCCCGGCTGCTCTCTCGCCGTG 727  
Qy 505 AAGTCTCGGGTATGCCCGCGCACGATGAGCCACTTTGACCCGTGGGACCCGCTCTCTCTT 564  
Db 728 CAGCTCACCGTGGCTGGCCATGTACTTGGCGTTCAACACCTGGGGCGCGCTACTCC 787  
Qy 565 CGCGCGGCTCGGCGCTCATGCTGCTGCGGTCTGGCGCTTCTTTCGCGCGTAC 624  
Db 788 CGCTTCGCGTCCACTTCGACCCCTACAGCCCATCTACGGCGACCGGGAGCGGCCAG 847  
Qy 625 GCGTACTCATCACTCGCTCGGCTTTCGGCT----- 656  
Db 848 ATCCCGCTCTCCGACGCGCGGCTCTGGCCGTGTCTGCGGTGTACAGGCTCGCGCG 907  
Qy 657 -----CATGGGCTCTACTACTATGCGCGCTCTTGTCTTCTTCTTCTG 699  
Db 908 GCCACCGGCTCTGGCCGCTGTGAGCGTCTACGGGTGCGCTGCTGTGACAAAGCC 967  
Qy 700 TTCTCTGCTATTACGACTTCTTTCACACAAACGACGAGCGCGCTGTGACGGGAC 759  
Db 968 TGGCTGTGGTGTGAGTCTGACACGACGCGCGGCTCCGCACTACGACTCC 1027  
Qy 760 TCGAGTGGAGTACGTCAAGGCAACTCTTCGAGCGTTCGACGCTGTACGGCGGCTTC 819  
Db 1028 AGCAGTGGAGTCTGATGCGCGGGGCTGCCACCGCTCGACCGGCTACGGGCTCTC 1087  
Qy 820 GTGACAACTTGAGCCACCAATTGGACGACCAAGTCCACCACTTGTTCCTCCCATTT 879  
Db 1088 AACCGGTGTTCACACCATCGCCGACAGCATATCGTCAACCATCTTTCCTGGCCATT 1147  
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Db 1148 CCGCACTACCAAGCATGAGGCGCACAGAGCATCGTCTCTCTCGGCGACTACTAC 1207  
Qy 940 CGCAGGACGACGAGCCCATCATCAGGCTTCT 973  
Db 1208 CGTCCGATAGCAGCCCATAGCGGAGCGCTCT 1241

## RESULT 15

US-10-437-963-68012  
; Sequence 68012, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 68012  
; LENGTH: 1317  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_68816C.1  
US-10-437-963-68012

Query Match 10.5%; Score 113; DB 19; Length 1317;  
Best Local Similarity 49.8%; Pred. No. 1e-21;  
Matches 413; Conservative 0; Mismatches 365; Indels 51; Gaps 3;  
Qy 191 TGTCTCCACGCGCTGTTTGGCCACCTACATCTACGTGACGGGGTGTATCTTCTGGGGCT 250  
Db 407 TCCTCCGCTCTGTCGCTGCGCTCTACTTGGGCGCGCAGGAGTGTACTACCGGCG 466  
Qy 251 TCTTACGCTGGCCACGACTCGGCGCACTCGGCTTCTCGCGTACACAGCTCAACT 310  
Db 467 TGTGGGTCACTGGGACAGAGTGTGGCCACACGCGCTTCTCGGACTACTTGTCTCGACA 526  
Qy 311 TTATCATCGGTGATCATGCACTCTCGGATTTTGACGCGTTCGAGAGCTGGCGCGTGA 370  
Db 527 ACCTCGTGGGCTAGTCTCACTCCGCGCTTCTCACGCGCTTCTTCTCGTGGAGTACA 586  
Qy 371 CGCACGCGCCACCAAGAACAGCGGCAACATTGATAGGAGGAGATCTTTTA---- 425  
Db 587 GCCACGCGCGCACCCGCCAACACCGGCTCCATGGAGAAAGAGAGTGTACGTCCGGA 646  
Qy 426 -----CCGCGACCGGTGCGTCAAGGACCTCCAGGACG 457  
Db 647 AGAAGAGTCCGCGCTGCGTGTACACCCCGTACGTTTCGGCAACCCCGTCCGGCGCG 706  
Qy 458 TGGCCCAATGGTCTACAGCTCGGCGTGGTGGTGTGTTGTTCTACTTGAAGTCCG----- 512  
Db 707 TGTGTATACATCGCGCTCGAGCTCACTCGGTGGCGCACTCTACTCGCGTTCAACTGT 766  
Qy 513 -----GTATGCCCCGCGACGATGAGCCACTTACCCGTTGACCCGTTGGGACCGCTCTCC 562  
Db 767 CCGGGAGCGTACCCACGCTGTCTACCTGCACTAGACCCCTACAGCCCGCTGTTC 826  
Qy 563 TTGCGCCGCGTGGCGC---GTATCGTGTGCTCGCGCTTGGGCGCGCTTCTTGGCGG 619  
Db 827 GCGACAGGAGCGGTCCAAGTCTCTCGACGCGCCATCTTGGCGGTGCTGTCTGCTCG 886  
Qy 620 GGTACGCGTACCTCAGATATCTCGCTCGGCTTTCGCGTATGGGCTCTACTACTATGGCG 679  
Db 887 CGTGTCAAGGCTGACGCGCGGTACGCGGCTCTGTTGGTGGTGTGCGGTGTACGGCGTGC 946  
Qy 680 CGCTCTTGTCTTGTCTTCT 739  
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Qy 740 CGACGCGGTGTACGCGGACTCTGGAGTGGAGTACGTCAAGGGCAACCTCTCGAGCGTGC 799  
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Qy 860 ACCACTTGTTCGCGATCATTTCCGCACTACAGCTCAACAGAGCCACCAAGCACTTTGGCG 919  
Db 1127 ACCACTCTTCCCCAGCATGCCACACTACCAACCGCATGGAGGCGCCAGGAGGAGGC 1186  
Qy 920 CCGGTATCCGCGACCTCGTGGCAGGAACGACAGCGCCCATCATCAGCGC 968  
Db 1187 CCGTCTCGGTGAGTACTACAGTTTTCACCGCACCGCCCATCATCGAGGC 1235

Search completed: October 11, 2005, 12:50:21  
Job time : 903 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 07:57:32 ; Search time 4887 Seconds

(without alignments)  
10678.590 Million cell updates/sec

Title: US-10-060-793A-25

Perfect score: 1077

Sequence: 1 atgactgagataagacgaa.....ccaaggccaagtggactaa 1077

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: gb\_ba:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1077	100.0	1077	8 AY373823	AY373823 Saprolegn
2	157	14.6	2090	6 E49240	E49240 Omega 3 fat
3	133	12.3	2485	1 SP036389	SP036389 Synchococ
4	131.2	12.2	1988	8 AB075527	AB075527 Chlorella
5	113	10.5	1089	6 AX653555	AX653555 Sequence
6	113	10.5	1267	8 AK105371	AK105371 Oryza sat
7	113	10.5	154025	8 AP005168	AP005168 Oryza sat
8	109.6	10.2	1518	8 D43688	D43688 Triticum ae
9	107.2	10.0	1549	6 E38843	E38843 Microsome 1
10	107.2	10.0	1595	6 E11610	E11610 cDNA encodi
11	107	9.9	1182	8 AY373822	AY373822 Saprolegn
12	107	9.9	1811	8 AK071185	AK071185 Oryza sat
13	105.8	9.8	662	6 E49247	E49247 Omega 3 fat
14	102.6	9.5	1494	8 D63953	D63953 Zea mays FA
15	102.2	9.5	1612	8 AK098930	AK098930 Oryza sat
16	102.2	9.5	1617	8 AK061531	AK061531 Oryza sat
17	101.2	9.4	1700	8 AK072282	AK072282 Oryza sat
18	101.2	9.4	123428	8 AP004098	AP004098 Oryza sat
19	101.2	9.4	172832	8 AP004047	AP004047 Oryza sat

20	100	9.3	1733	6	BD234746	Desaturas
21	99.6	9.2	1856	8	AK052339	Oryza sat
22	98.6	9.2	1203	8	AF417244	Mortierel
23	98.6	9.2	1203	8	AF417245	Mortierel
24	97.6	9.1	1725	1	SYCDESB	SYCDESB
25	97.6	9.1	143308	1	D90913	Synechocyst
26	96	8.9	2247	8	AB007640	Chlamydom
27	94.4	8.8	1590	8	D84678	Triticum ae
28	93.8	8.7	1427	8	AB075526	AB075526
29	93.6	8.7	302550	1	AP006581	Chlorella
30	93.4	8.7	1302	1	AF134896	AF134896
31	93.4	8.7	297850	1	AP006577	AP006577 Gloeobact
32	92.8	8.6	1177	8	AK061506	AK061506 Oryza sat
33	91.6	8.5	1146	6	BD235521	BD235521 Desaturas
34	91.6	8.5	1790	6	BD234745	BD234745 Desaturas
35	91.6	8.5	1790	6	AR207489	AR207489 Sequence
36	91.6	8.5	6337	6	BD235520	BD235520 Desaturas
37	90.8	8.4	1245	6	AX654569	AX654569 Sequence
38	88.4	8.2	1297	8	AF182521	AF182521 Momordica
39	88.4	8.2	1308	6	BD224596	BD224596 Genes for
40	85.8	8.0	1403	8	AB020033	AB020033 Mortierel
41	82.8	7.7	1037	8	AY581826	AY581826 Cynodon d
42	82.4	7.7	110000	8	AE016819	Continuation (15 o
43	82	7.6	1200	6	BD232181	BD232181 Compositi
44	82	7.6	1488	6	AR080599	AR080599 Sequence
45	82	7.6	1488	6	AR098440	AR098440 Sequence

#### ALIGNMENTS

RESULT 1  
AY373823  
LOCUS  
DEFINITION Saprolegnia diclina omega-3 fatty acid desaturase (sdd17) mRNA,  
complete cds.  
1077 bp mRNA linear PLN 05-MAY-2004  
AY373823  
ACCESSION AY373823.1 GI:38426732  
VERSION  
KEYWORDS  
SOURCE Saprolegnia diclina  
ORGANISM Saprolegnia diclina  
Eukaryota; stramenopiles; Oomycetes; Saprolegniales;  
Saprolegniaceae; Saprolegnia.  
1 (bases 1 to 1077)  
Pereira,S.L., Huang,Y.S., Bobik,E.G., Kinney,A.J., Stecca,K.L.,  
Packer,J.C. and Mukerji,P.  
A novel omega3-fatty acid desaturase involved in the biosynthesis  
of eicosapentaenoic acid  
Biochem. J. 378 (Pt 2), 665-671 (2004)  
14651475  
2 (bases 1 to 1077)  
Pereira,S.L., Mukerji,P. and Huang,Y.-S.  
Direct Submission  
Submitted (25-AUG-2003) 104060, Abbott Laboratories-Ross Products  
Division, RP4-3, 3300 Stelzer Road, Columbus, OH 43219, USA  
Location/Qualifiers  
1. .1077  
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/mol\_type="mRNA"  
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1. .1077  
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1. .1077  
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ASALLYAAKSTFTFIADNVLLHALVCATYIVQGVIFWGFTVGHDCGHSFSAFVHSV



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 11, 2005, 07:58:42 ; Search time 4079 Seconds

(without alignments)

10050.311 Million cell updates/sec

Title: US-10-060-793a-25

Perfect score: 1077

Sequence: 1 atgactgagataagacgaa.....ccaaagccaagtcggaactaa 1077

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.\*

1: gb\_est1.\*

2: gb\_est2.\*

3: gb\_hic.\*

4: gb\_est3.\*

5: gb\_est4.\*

6: gb\_est5.\*

7: gb\_est6.\*

8: gb\_gssi.\*

9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	357.4	33.2	664	7	CF840561
2	273	25.3	597	7	CF850773
3	240.2	22.3	643	2	BE777235
4	222.8	20.7	683	2	BE776116
5	111.2	10.3	1520	3	AY107103
6	102.8	9.5	714	7	CF866439
7	102.8	9.5	770	6	CB9896410
8	101.6	9.4	1636	3	AY111307
9	101.4	9.4	700	7	CF877405
10	101.4	9.4	744	7	CF866831
11	101.4	9.4	754	6	CB905755
12	101.4	9.4	799	6	CB9896826
13	101.2	9.4	749	4	BN076378
14	100.6	9.3	743	9	CC672052
15	99.6	9.2	614	7	CF944131
16	99.6	9.2	737	7	CF869634
17	99.6	9.2	747	7	CF877651
18	99.6	9.2	753	7	CF877603
19	99.6	9.2	794	6	CB899781
20	99.6	9.2	803	6	CB905880
21	99.6	9.2	810	6	CB905819
22	99.4	9.2	577	6	CB874512
23	98	9.1	648	6	CB307629
24	97.6	9.1	519	7	CO750847

25	97	9.0	776	9	CL187144
26	96.4	9.0	526	7	CV061040
27	96.4	9.0	550	5	BU977672
28	96.4	9.0	559	4	BJ448151
29	96.4	9.0	592	4	BJ481919
30	96.4	9.0	592	7	CV061475
31	96.4	9.0	789	2	BF621168
32	96.4	9.0	850	4	BM816152
33	96.4	9.0	885	4	BM816153
34	96	8.9	626	7	CV061550
35	96	8.9	751	7	CV064038
36	95.4	8.9	688	6	CD231034
37	95.4	8.9	800	7	CN138596
38	95	8.8	826	9	CG438073
39	93.8	8.7	852	7	CN145070
40	92.2	8.6	763	6	CB903019
41	92.2	8.6	763	7	CF872996
42	92.2	8.6	1165	7	CK211148
43	92	8.5	655	6	CD903989
44	91.6	8.5	1084	7	CK210592
45	91.6	8.5	1856	3	AY104050

#### ALIGNMENTS

RESULT 1  
CF840561  
LOCUS  
DEFINITION pSHB009xD12f USDA-IPAFS:Expression of Phytophthora sojae genes during infection and propagation\_sHB  
SHB009D12 5, mRNA sequence.  
ACCESSION CF840561  
VERSION CF840561.1  
KEYWORDS EST.  
SOURCE Phytophthora sojae  
ORGANISM Phytophthora sojae  
REFERENCE 1 (bases 1 to 664)  
AUTHORS Tyler, B.  
TITLE Tyler, B. Not Published  
JOURNAL Unpublished (2003)  
COMMENT Contact: Tyler B  
Tyler lab  
VBI

1880 Pratt Dr., Blacksburg, VA 24061, USA  
Tel: 540-231-7318  
Email: bmtyle@vt.edu  
PCR Primers  
FORWARD: BK reverse primer  
BACKWARD: BK reverse primer  
Plate: 009 row: D column: 12  
Seq primer: BK reverse primer  
High quality sequence stop: 664.  
Location/Qualifiers  
1. 664  
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/dev\_stage="48 hr. post infection stage"  
/lab\_host="Soybean plant"  
/clone\_lib="USDA-IPAFS:Expression of Phytophthora sojae genes during infection and propagation\_sHB"  
/note="vector: pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI"

#### FEATURES

source  
Query Match 33.2%; Score 357.4; DB 7; Length 664;  
Best Local Similarity 71.6%; Pred No. 1e-72;  
Matches 469; Conservative 0; Mismatches 186; Indels 0; Gaps 0;  
ORIGIN







XX The invention is directed to the identification and isolation of novel  
CC genes that encode enzymes involved in the synthesis of polyunsaturated  
CC fatty acids (PUFAs). In particular the invention is directed to genes  
CC derived from the fungus *Saprolegnia diclina* that encode omega-3  
CC desaturase (also referred to as delta-17 desaturase) and delta-12  
CC desaturase. Polynucleotides, composition and methods of the invention are  
CC useful for preventing or treating conditions caused by insufficient  
CC intake of at least one PUFA e.g. eczema, burned or dry skin, acquired  
CC immune deficiency syndrome (AIDS), multiple sclerosis or inflammatory  
CC skin disorders. Products produced in the method of the invention are  
CC useful in pharmaceutical and nutritional compositions, animal feeds and  
CC cosmetics. The invention is also useful in gene therapy. The present  
CC sequence is *Saprolegnia diclina* omega-3 desaturase gene  
XX  
SQ Sequence 1077 BP; 191 A; 379 C; 286 G; 221 T; 0 U; 0 Other;

Query Match 100.0%; Score 1077; DB 10; Length 1077;

Best Local Similarity 100.0%; Pred. No. 6.2e-219;

Matches 1077; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATGACTGAGTATAGACGAGGTGCGAGTTCCCGACGCTCAGGAGCTCAAGCACTCGATC	60
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Qy	61	CCGAACCGGTCTTGTAGTTCGAACCTCGGCTCTCTGCTCTACTACACGGCCCGCGGATC	120
Db	61	CCGAACCGGTCTTGTAGTTCGAACCTCGGCTCTCTGCTCTACTACACGGCCCGCGGATC	120
Qy	121	TTCAACCGCTCGGCTCGGCGGCTCTCTACGCGCGGCTCGACGCCGTTTCATTGCC	180
Db	121	TTCAACCGCTCGGCTCGGCGGCTCTCTACGCGCGGCTCGACGCCGTTTCATTGCC	180
Qy	181	GATAAGCTTCTGCTCAGCGGCTGTTTGGCCACCTACTACTAGTTCGAGGGGCTCATC	240
Db	181	GATAAGCTTCTGCTCAGCGGCTGTTTGGCCACCTACTACTAGTTCGAGGGGCTCATC	240
Qy	241	TTCTGGGGCTTCTTTCAGGTCGGCCAGCTCGGGCCACTCGGCTTCTCGCGTACCAC	300
Db	241	TTCTGGGGCTTCTTTCAGGTCGGCCAGCTCGGGCCACTCGGCTTCTCGCGTACCAC	300
Qy	301	AGCGTCAACTTATCATCGGCTGCATCATGCACTCTCGGATTTTACGCCGTTTCGAGAGC	360
Db	301	AGCGTCAACTTATCATCGGCTGCATCATGCACTCTCGGATTTTACGCCGTTTCGAGAGC	360
Qy	361	TGGCGGTGACGACCCGCCACCAACCAAGAACACGGGCAACATTGATAGGACGATC	420
Db	361	TGGCGGTGACGACCCGCCACCAACCAAGAACACGGGCAACATTGATAGGACGATC	420
Qy	421	TTTATCCCGCACCGGTCGGTCAAGGACTTCAGGACCTCGGCAATGGGTCTACACGCTC	480
Db	421	TTTATCCCGCACCGGTCGGTCAAGGACTTCAGGACCTCGGCAATGGGTCTACACGCTC	480
Qy	481	GGCGGTGCGTGGTGTGTACTTGAAGGTGGGTPATGCCCGCGCACGATGAGCACTTT	540
Db	481	GGCGGTGCGTGGTGTGTACTTGAAGGTGGGTPATGCCCGCGCACGATGAGCACTTT	540
Qy	541	GACCGGTGGGACCGGCTCTCTTCGCGCGGCTCGCGGCTCATCGTGTGCTCGGCGTC	600
Db	541	GACCGGTGGGACCGGCTCTCTTCGCGCGGCTCGCGGCTCATCGTGTGCTCGGCGTC	600
Qy	601	TGGCGCGCTTCTTTCGCGGCTAGCGGTACTCTACATACTCGCTCGGCTTTCGCGTCATG	660
Db	601	TGGCGCGCTTCTTTCGCGGCTAGCGGTACTCTACATACTCGCTCGGCTTTCGCGTCATG	660
Qy	661	GGCCTCTACTACTATGCGCGCTCTTGTCTTTCGCTTTCGCTCGTTCATTAGACCTTC	720
Db	661	GGCCTCTACTACTATGCGCGCTCTTGTCTTTCGCTTTCGCTCGTTCATTAGACCTTC	720
Qy	721	TTGCACACACGACGACGACCGCTGTTACGGGACTCGGAGCTGAGTACGTCAAG	780
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Db	901	GCCACCAAGCACATTTTCGGCGCGGTACCGGACCTCTGTGCGCAGGAAACGAGCCCATC	960
Qy	961	ATCACGGCTTCTTCAAGACCGCGCACCTCTTTGTCAACTACGCGGCTGTGCCGAGACG	1020
Db	961	ATCACGGCTTCTTCAAGACCGCGCACCTCTTTGTCAACTACGCGGCTGTGCCGAGACG	1020
Qy	1021	GCGCAGATCTTCAAGCTCAAGAGTGGCGCGCGGCCCAAGGCCAAAGTCGGACTAA	1077
Db	1021	GCGCAGATCTTCAAGCTCAAGAGTGGCGCGCGGCCCAAGGCCAAAGTCGGACTAA	1077

RESULT 2  
ADR20168  
ID ADR20168 standard; cDNA; 1077 BP.  
XX  
AC ADR20168;  
XX AC  
DT 18-NOV-2004 (first entry)  
XX  
DE DE  
KW Saprolegnia diclina delta-17 desaturase encoding cDNA SEQ ID NO:41.  
KW oilseed plant; mature seed; seed fatty acid profile;  
KW polyunsaturated fatty acid; delta-17 desaturase; oil; food; food product;  
KW beverage; infant formula; nutritional supplement; pet food; animal feed;  
KW whole bean soy product; aquaculture food product; enzyme; gene; ss.  
XX  
OS Saprolegnia diclina.  
XX  
PH Key Location/Qualifiers  
FT CDS 1..1077  
FT /\*tag= a /product= "delta-17 desaturase"  
XX  
PN WO2004071467-A2.  
XX  
PD 26-AUG-2004.  
XX  
PF 12-FEB-2004; 2004WO-US005758.  
XX  
PR 12-FEB-2003; 2003US-0446941P.  
XX  
PA (DUPO ) DU PONT DE NEMOURS & CO E I.  
XX  
PI Kinney AU, Cahoon EB, Damude HG, Hitz WD, Kolar CW, Liu Z;  
XX  
PI WPI; 2004-625770/60.  
XX  
DR P-PSDB; ADR20169.  
XX  
DR  
XX  
PT Novel oilseed plant useful for mature seeds in which total seed fatty  
PT acid profile comprises high polyunsaturated fatty acid.  
XX  
XX  
PS Example 3; SEQ ID NO 41; 132pp; English.  
XX  
CC The present invention describes an oilseed plant (I) that produces mature  
CC seeds in which the total seed fatty acid profile comprises at least 1.0%,  
CC 5%, 10%, 15%, 20%, 25%, 30%, 40%, 50%, 60% or more of at least one  
CC polyunsaturated fatty acid having 20 or more carbon atoms and 5 or more  
CC carbon-carbon double bonds, and ratio of docosahexaenoic  
CC acid:eicosapentaenoic acid (DHA:EPA) is 1:100-860:100 or 1:100-110:100,  
CC where total seed fatty acid profile further comprises less than 2%  
CC arachidonic acid. Also described: (1) seeds (II) obtained from (I); (2)  
CC oil (III) obtained from (II); (3) a recombinant construct (IV) for  
CC altering the total fatty acid profile of mature seeds of an oilseed

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	91.6	8.5	1790	3	US-09-133-962A-7	Sequence 7, Appli
2	82	7.6	1488	2	US-08-834-655-3	Sequence 3, Appli
3	82	7.6	1488	3	US-08-834-033A-3	Sequence 3, Appli
4	82	7.6	1488	3	US-09-363-574-3	Sequence 3, Appli
5	82	7.6	1488	3	US-09-363-526-3	Sequence 3, Appli
6	82	7.6	1488	3	US-09-330-235-19	Sequence 19, Appli
7	72.2	6.7	1155	3	US-08-907-608-5	Sequence 5, Appli
8	72.2	6.7	1155	3	US-09-354-231B-5	Sequence 5, Appli
9	72.2	6.7	1155	3	US-09-128-602B-5	Sequence 5, Appli
10	72.2	6.7	1155	3	US-09-482-287-5	Sequence 5, Appli
11	72.2	6.7	1155	4	US-09-966-888-5	Sequence 5, Appli
12	72.2	6.7	1155	4	US-09-995-297-5	Sequence 5, Appli
13	70.6	6.6	1155	3	US-08-907-608-3	Sequence 3, Appli
14	70.6	6.6	1155	3	US-09-354-231B-7	Sequence 7, Appli
15	70.6	6.6	1155	3	US-09-128-602B-7	Sequence 7, Appli
16	70.6	6.6	1155	3	US-09-482-287-3	Sequence 3, Appli
17	70.6	6.6	1155	4	US-09-966-888-3	Sequence 3, Appli
18	70.6	6.6	1155	4	US-09-995-297-7	Sequence 7, Appli
19	70.6	6.6	1231	1	US-08-314-596-44	Sequence 44, Appli
20	70.6	6.6	1231	1	US-08-320-982-44	Sequence 44, Appli
21	70.6	6.6	1231	3	US-08-819-037-44	Sequence 44, Appli
22	70.6	6.6	1231	3	US-09-045-940-44	Sequence 44, Appli
23	70.6	6.6	1372	3	US-09-133-962A-1	Sequence 1, Appli
24	70.6	6.6	1372	4	US-09-763-331-5	Sequence 5, Appli
25	70.6	6.6	2973	3	US-09-133-962A-15	Sequence 15, Appli
26	68.2	6.3	1155	2	US-08-675-650B-5	Sequence 5, Appli
27	67.4	6.3	1128	3	US-09-161-994A-1	Sequence 1, Appli

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CLONE: pFad2#1
FEATURE:
NAME/KEY: CDS
LOCATION: 165..1328
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-133-962A-7

Query Match      8.5%; Score 91.6; DB 3; Length 1790;
Best Local Similarity 47.8%; Pred. No. 1.3e-12;
Matches 412; Conservative 0; Mismatches 399; Indels 51; Gaps 3;

Qy 96 GCTCTACTACACGCCCGCGCATCTTTCAACGGCTCGGCTCGGCGCGCTGCTCTACGC 155
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Qy 329 GCTCAAGTCTTCTCGTACGTGGTCCACGACCTGGTGATCGCGCGCGCTCCTTACTT 388
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Qy 156 GCGCGCTCGACGCCGTTCAATGCCGATAAGTTCTGCTCAGCGCGTCTGTTGCGGCAC 215
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 389 CGCGCTGGCCATCATACCGCGCTCCCAAGCCGCTCCGCTACGC---CGCCTGGCGCT 445
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 216 CTACATCTAGTGCAGGGCGTCTATCTTCTGGGCTTCTTACAGTGGGCCACGACTGCGG 275
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 446 GTACTGATCGCGAGGGGTGCGTGTGACCGGGTGTGGTATCGCGCACGAGTGGG 505
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Qy 276 CCACTCGGCTTCTCGCGCTACCAACGCTCAACTTATCATCGGCTGCATGCACTC 335
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Qy 336 TGGATTTTACGCGCTTTCAGAGCTGGCGGGTGAACGACCGGCCACCAACAAGAACAC 395
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Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Qy 507 -----GGTGGGTATGCCCGGCGGAGAT 530
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 531 GAGCACTTTGACCGGTGGACCGCTCTCTTTCGCGCGCGTGGCGC---GTCACTGT 587
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Qy 888 CAAGCTCAAGGACCAACCAAG 909
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US-08-834-655-3
; Sequence 3, Application US/08834655
; Patent No. 5968809
; GENERAL INFORMATION:
; APPLICANT: KNUTZON, DEBORAH
; APPLICANT: MURKERJI, PRADIP
; APPLICANT: HUANG, YUNG-SHENG
; APPLICANT: THURMOND, JENNIFER
; APPLICANT: CHAUDHARY, SUNITA
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR SYNTHESIS
; OF LONG CHAIN POLY-UNSATURATED FATTY ACIDS IN PLANTS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RAE-VENTER LAW GROUP, P.C.
; STREET: 260 SHERIDAN AVENUE, P.O. BOX 60039
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94306
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/834,655
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RAE-VENTER, BARBARA
; REGISTRATION NUMBER: 32,750
; REFERENCE/DOCKET NUMBER: CGNE.124.00US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 328-4400
; TELEFAX: (650) 328-4477
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1488 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-834-655-3
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Query Match      7.6%; Score 82; DB 2; Length 1488;
Best Local Similarity 54.2%; Pred. No. 2.5e-10;
Matches 166; Conservative 0; Mismatches 140; Indels 0; Gaps 0;

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Qy 183 TAAAGTTCTCTCCACGCGCTCGTTTTCGCGCACCTACATCTACGTGAGGCGGTCACTTT 242
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Qy 426 GAATCCCTTGATCCGCTATTGTGCTGGCTGCTTACTGGATCATGAGGATTTGCTG 485
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Qy 243 CTGGGCTTCTTCCAGTGGCGCACGCTCGGCGCGCTCGGCGCTTCTCGCGCTACCACAG 302
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 486 CACCGGTGTCTGGGTGCTGGCTCACGAGTGTGTCTAGTCTCTCTCGACCTCCAAGAC 545
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 303 CGTCAACTTTTATCATCGGCTGTCATCATGCACTCTGCGATTTTGACGCGCTTCGAGAGCTG 362
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 546 CCTCAACACACAGTTGGTTGGATCTTGCACTCGATGCTCTTGGTCCCTACCACCTCTG 605
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 363 GCGGTGACGACCGCGCACCGCACCAAGAAACAGGGCAACATTGATGAAGACGAGATCTT 422
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 606 GAGAACTCGCACTCGAAGCACCAAGGCACTGGGCCATATGACCAAGGACCGAGTCTT 665
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 423 TTACCC 428
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 666 TGTGCC 671
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 11, 2005, 06:12:48 ; Search time 2675 Seconds  
(without alignments)  
932.117 Million cell updates/sec

Title: US-10-060-793A-26

Perfect score: 1929

Sequence: 1 MTEDTKVVEPTTELKHSI.....ETRAQIFLKESAAAAAKSD-358

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Delop 6.0 , Delext 7.0	

Searched: 8443130 seqs, 3482420727 residues

Total number of hits satisfying chosen parameters: 16886260

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
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Database :

Published Applications NA:\*

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- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
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- 10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*
- 11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*
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- 24: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*
- 25: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*
- 26: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1929	100.0	1077	16	US-10-060-793-25	Sequence 25, Appl
2	1929	100.0	1077	19	US-10-776-311-41	Sequence 41, Appl
3	1929	100.0	1077	20	US-10-840-478-3	Sequence 3, Appli
4	1929	100.0	1077	21	US-10-840-325-35	Sequence 35, Appl
5	1929	100.0	1077	22	US-10-840-579-5	Sequence 5, Appli
6	1929	100.0	12456	22	US-10-985-109-95	Sequence 95, Appl
c	1929	100.0	12456	22	US-10-985-109-95	Sequence 95, Appl
8	1924	99.7	1077	20	US-10-840-478-62	Sequence 46, Appl
9	1924	99.7	1077	21	US-10-840-325-46	Sequence 101, App
10	1924	99.7	1077	22	US-10-840-579-9	Sequence 9, Appli
11	1924	99.7	10328	21	US-10-840-325-129	Sequence 129, App
12	1924	99.7	10328	22	US-10-840-579-101	Sequence 101, App
13	586.5	30.4	1080	17	US-10-369-493-26432	Sequence 26432, A
14	586.5	30.4	2001	17	US-10-310-154-101	Sequence 101, App
15	586.5	30.4	2001	21	US-10-732-923-186	Sequence 186, App
16	582	30.2	999	17	US-10-369-493-42763	Sequence 42763, A
17	572.5	29.7	1041	17	US-10-369-493-43786	Sequence 43786, A
18	529	27.4	1955	20	US-10-425-115-126240	Sequence 126240, A
19	527	27.3	1666	20	US-10-425-115-126274	Sequence 126274, A
20	523.5	27.1	1242	20	US-10-491-733-7	Sequence 7, Appli
21	522.5	27.1	1405	19	US-10-419-865-3	Sequence 3, Appli
22	516.5	26.8	1543	20	US-10-604-708-10	Sequence 10, Appl
23	516.5	26.8	1900	17	US-10-310-154-98	Sequence 98, Appl
24	516.5	26.8	1900	21	US-10-732-923-20	Sequence 20, Appl
25	514.5	26.7	1553	20	US-10-425-115-81874	Sequence 81874, A
26	512	26.5	1279	21	US-10-487-901-62236	Sequence 62236, Ap
27	510	26.4	1308	9	US-09-938-842A-635	Sequence 635, App
28	510	26.4	1308	11	US-09-938-842A-635	Sequence 635, App
29	510	26.4	1525	17	US-10-310-154-100	Sequence 100, App
30	510	26.4	1525	21	US-10-732-923-22	Sequence 22, Appl
c	509.5	26.4	1496	18	US-10-424-599-72596	Sequence 72596, A
31	508.5	26.4	1461	18	US-10-424-599-53502	Sequence 53502, A
32	506.5	26.3	1376	19	US-10-419-865-4	Sequence 4, Appli
33	506.5	26.3	1395	19	US-10-419-865-5	Sequence 5, Appli
34	506.5	26.3	1976	19	US-10-437-963-25531	Sequence 25531, A
35	505.5	26.2	1847	18	US-10-424-599-116485	Sequence 116485, A
36	505.5	26.1	1350	19	US-10-776-311-47	Sequence 47, Appl
37	503	26.1	1475	16	US-10-165-289A-7	Sequence 7, Appli
38	503	26.1	2318	18	US-10-424-599-116486	Sequence 116486, A
39	499.5	25.9	1662	17	US-10-310-154-99	Sequence 99, Appl
40	499.5	25.9	1662	21	US-10-732-923-21	Sequence 21, Appl
41	497	25.8	1142	16	US-10-115-571A-7	Sequence 7, Appli
42	492.5	25.5	1766	20	US-10-739-930-2687	Sequence 2687, Ap
43	492.5	25.5	1152	19	US-10-772-227-25	Sequence 25, Appl
44	492	25.5	1152	22	US-10-912-534-25	Sequence 25, Appl
45	492	25.5	1152	22	US-10-912-534-25	Sequence 25, Appl

#### ALIGNMENTS

RESULT 1

US-10-060-793-25  
; Sequence 25, Application US/10060793  
; Publication No. US20030196217A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pradip  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Pereira, Suzette L.  
; TITLE OF INVENTION: DESATURASE GENES, ENZYMES ENCODED  
; TITLE OF INVENTION: THEREBY, AND USES THEREOF  
; FILE REFERENCE: 6884.US.O1  
; CURRENT APPLICATION NUMBER: US/10/060.793  
; CURRENT FILING DATE: 2002-06-24  
; NUMBER OF SEQ ID NOS: 60  
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 25
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Saprolegnia diclina
US-10-060-793-25

Alignment Scores:
Pred. No.: 5,04e-226 Length: 1077
Score: 1929.00 Matches: 358
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 16 Gaps: 0

US-10-060-793A-26 (1-358) x US-10-060-793-25 (1-1077)

Qy 1 MetThrGluAspLysThrIysValGluPheProThrLeuThrGluLeuLysHisSerIle 20
Db 1 ATGACTGAGGATAAGACGAAGGTCGAGTCCCGACGCTACGGAGCTCAAGCACTCGATC 60
Qy 21 ProAsnAlaCysPheGluSerAsnLeuGlyLeuSerLeuTyrThrAlaArgAlaIle 40
Db 61 CCAGACGCGTCTTGGTGGTGAACCTCGGCTCTCGCTCTACTACACGCGCGCGATC 120
Qy 41 PheAsnAlaSerAlaSerAlaAlaLeuLeuTyrAlaAlaArgSerThrProPheIleAla 60
Db 121 TTCAACGCGTCTCGGCGCGGCTGCTCTAGCGCGCGCTCGACCGCGCTCATGTGCC 180
Qy 61 AspAsnValLeuLeuHisAlaLeuValCysAlaThrTyrIleTyrValGlnGlyValIle 80
Db 181 GATAACGCTTCTTCAACGCGTCTCGGCGCGGCTGCTCTAGCGCGCGCTCGACCGCTCATC 240
Qy 81 PheTrpGlyPheThrValGlyHisAspCysGlyHisSerAlaPheSerArgTyrHis 100
Db 241 TTCTGGGCGTCTTCAACGCGTCTCGGCGCGGCTGCTCTAGCGCGCGCTCGACCGCTCATC 300
Qy 101 SerValAsnPheIleIleGlyCysIleMetHisSerAlaIleLeuThrProPheGluSer 120
Db 301 AGCGTCNACTTTATCATCGCTGTCATCATCGACTCTGCGATTTTGGCGGCTTCGAGAGC 360
Qy 121 TrpArgValThrHisArgHisHisLysAsnThrGlyAsnIleAspLysAspGluIle 140
Db 361 TGGCGCGTGCAGCACCGCCACCAACCAAGAACACCGGCAACATTTGATAAGGACGAGATC 420
Qy 141 PheTyrProHisArgSerValIysAspLeuGlnAspValArgGlnTrpValTyrThrLeu 160
Db 421 TTTTACCCGACCGCGTCTCTTCTCGCGCGCGTCTCGGCGCGCTCATCGTCTCGGCGTC 480
Qy 161 GlyGlyAlaTrpPheValTyrLeuLysValGlyTyrAlaProArgThrMetSerHisPhe 180
Db 481 GCGGCTGCGTGGTTTGTCTACTTGAAGTCTGGGTATGCCCGCGCACGATGAGCCACTTT 540
Qy 181 AspProTrpAspProLeuLeuLeuArgAlaSerAlaValIleValSerLeuGlyVal 200
Db 541 GACCCGCGGACCGCTCTCTTCTCGCGCGCGTCTCGGCGCGCTCATCGTCTCGGCGTC 600
Qy 201 TrpAlaAlaPhePheAlaAlaTyrAlaTyrLeuThrTyrSerLeuGlyPheAlaValMet 220
Db 601 TGGCGCGCTCTTCTCGCGCGGTACGGGTACCTCACATCTCGTCTGGCTTTGCGGTCATG 660
Qy 221 GlyLeuTyrTyrTrpAlaProLeuPheValPheAlaSerPheLeuValIleThrThrPhe 240
Db 661 GGCTCTACTATGTCGCGCGCTCTTGTCTTGTCTTGTCTCTCTCTCTCTCTCTCTCTCTCT 720
Qy 241 LeuHisHisAsnAspGluAlaThrProTrpTyrGlyAspSerGluTrpThrThrValLys 260
Db 721 TTGCACCAACACGACGAAGCGACCGCTGTCGCGGCTCTCGGACCTCGGACCTACGTCAG 780
Qy 261 GlyAsnLeuSerSerValAspArgSerTyrGlyAlaPheValAspAsnLeuSerHisHis 280
Db 781 GGAACCTCTCGAGCGTCTGACCGCTCTGACGGCGCTCTGAGCAACCTCGAGCCACAC 840
Qy 281 IleGlyThrHisGlnValHisHisLeuPheProIleIleProHisTyrLysLeuAsnGlu 300
Db 301 AGCGTCAACTTTATCATCGCTGTCATCATGCTCTGCGATTTTGACGCGCTTCGAGAGC 360

; SEQ ID NO 25
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Saprolegnia diclina
US-10-060-793A-26 (1-358) x US-10-060-793-311 (1-1077)

Alignment Scores:
Pred. No.: 5,04e-226 Length: 1077
Score: 1929.00 Matches: 358
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 19 Gaps: 0

US-10-060-793A-26 (1-358) x US-10-060-793-311-41 (1-1077)

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Db 1 ATGACTGAGGATAAGACGAAGGTCGAGTTCGCCAGCTCACGGAGCTCAAGCACTCGATC 60
Qy 21 ProAsnAlaCysPheGluSerAsnLeuGlyLeuSerLeuTyrThrAlaArgAlaIle 40
Db 61 CCAGACGCGTCTTGGTGGTGAACCTCGGCTCTCGCTCTACTACACGCGCGCGATC 120
Qy 41 PheAsnAlaSerAlaSerAlaAlaLeuLeuTyrAlaAlaArgSerThrProPheIleAla 60
Db 121 TTCAACGCGTCTCGGCGCGGCTGCTCTAGCGCGCGCTCGACCGCGCTCATGTGCC 180
Qy 61 AspAsnValLeuLeuHisAlaLeuValCysAlaThrTyrIleTyrValGlnGlyValIle 80
Db 181 GATAACGCTTCTTCAACGCGTCTCGGCGCGGCTGCTCTAGCGCGCGCTCGACCGCTCATC 240
Qy 81 PheTrpGlyPheThrValGlyHisAspCysGlyHisSerAlaPheSerArgTyrHis 100
Db 241 TTCTGGGCGTCTTCAACGCGTCTCGGCGCGGCTGCTCTAGCGCGCGCTCGACCGCTCATC 300
Qy 101 SerValAsnPheIleIleGlyCysIleMetHisSerAlaIleLeuThrProPheGluSer 120
Db 301 AGCGTCAACTTTATCATCGCTGTCATCATGCTCTGCGATTTTGGCGGCTTCGAGAGC 360

; Sequence 41, Application US/10776311
; Publication No. US20040172692A1
; GENERAL INFORMATION:
; APPLICANT: Edgar B. Cahoon
; APPLICANT: Howard G. Damude
; APPLICANT: William D. Hitz
; APPLICANT: Anthony J. Kinney
; APPLICANT: Charles W. Kolar
; APPLICANT: Zhan Bin Liu
; TITLE OF INVENTION: Production of Long Chain Polyunsaturated Fatty Acids in Plants
; FILE REFERENCE: B01538 US NA
; CURRENT APPLICATION NUMBER: US/10776,311
; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: US 60/446,941
; PRIOR FILING DATE: 2003-02-12
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Saprolegnia diclina
US-10-060-793-311-41
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 11, 2005, 06:12:42 ; Search time 5425 Seconds

(without alignments)  
3197.598 Million cell updates/sec

Title: US-10-060-793A-26

Perfect score: 1929

Sequence: 1 MTEDKTKVPEPTTELKHSI.....ETAIQIFLKESAAAAAKAKSD 358

Scoring table:

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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
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-FGAEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: gb.btg.\*  
3: gb.in.\*  
4: gb.om.\*  
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6: gb.pat.\*  
7: gb.ph.\*  
8: gb.pl.\*  
9: gb.pr.\*  
10: gb.ro.\*  
11: gb.ets.\*  
12: gb.ey.\*  
13: gb.un.\*  
14: gb.vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	587.5	30.5	349050	1 AP003586	AP003586 Nostoc sp
3	586.5	30.4	1725	1 SYCD85B	D13780 Synechocyst
c 4	586.5	30.4	143308	1 D90913	D90913 Synechocyst

5	577.5	29.9	1762	1	AJ621246	AJ621246 Nostoc sp
6	538.5	27.9	2090	6	E49240	E49240 Omega 3 fat
7	530	27.5	1494	8	D63953	D63953 Zea mays FA
8	529	27.4	2248	8	PAB302017	AJ302017 Picea abi
9	528	27.4	1308	8	AY248741	AY248741 Lycopersi
10	527	27.3	2485	1	SPU36389	U36389 Synechococc
11	525	27.2	1180	8	AY204711	AY204711 Glycine m
12	525	27.2	1546	8	STU007739	AU007739 Solanum t
13	523.5	27.1	1612	8	AK098930	AK098930 Oryza sat
14	523.5	27.1	1617	8	AK061531	AK061531 Oryza sat
15	522.5	27.1	1320	8	AY551558	AY551558 Malus x d
16	521	27.0	1143	8	AB105886	AB105886 Glycine m
17	521	27.0	1308	8	AY157317	AY157317 Lycopersi
18	521	27.0	1366	8	TOBNTFAD3	D6509 Tobacco lea
19	521	27.0	2181	6	AR074344	AR074344 Sequence
20	521	27.0	1675	6	SOYCFGAD3A	L22964 Glycine soj
21	520.5	27.0	1675	6	AR074345	AR074345 Sequence
22	520.5	27.0	1675	8	SOYCFPADD	L22965 Glycine soj
23	518	26.9	1958	8	RCCPAD7A	L25897 Ricinus com
24	515	26.7	1703	8	AY135565	AY135565 Betula pe
25	514.5	26.7	998	8	AB188198	AB188198 Glycine m
26	514.5	26.7	1178	8	AY599884	AY599884 Braesica
27	514	26.6	1245	6	AX654569	AX654569 Sequence
28	514	26.6	1556	8	PCU75745	U75745 Petroselinu
29	514	26.6	1606	8	D79979	D79979 Nicotiana t
30	513	26.6	1889	8	AY135564	AY135564 Betula pe
31	510.5	26.5	1588	8	AY135566	AY135566 Betula pe
32	510	26.4	1308	6	AX505940	AX505940 Sequence
33	510	26.4	1308	6	AX651646	AX651646 Sequence
34	510	26.4	1308	8	AY078043	AY078043 Arabidops
35	510	26.4	1402	8	AY093304	AY093304 Arabidops
36	510	26.4	1525	8	ATHFAD8A	L27158 Arabidopsis
37	510	26.4	1605	8	AY062468	AY062468 Arabidops
38	510	26.4	1621	8	ATHFADIP1	D17578 Arabidopsis
39	510	26.4	1656	8	AF361837	AF361837 Arabidops
40	508.5	26.4	1131	8	AB105887	AB105887 Glycine m
41	508.5	26.4	1216	8	AY204712	AY204712 Glycine m
42	508.5	26.4	1350	8	AF020204	AF020204 Petargoni
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ALIGNMENTS

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LOCUS	AY373823	Saprolignia diclina omega-3 fatty acid desaturase (sdd17) mRNA,			
DEFINITION	AY373823	complete cds.			
ACCESSION	AY373823	AY373823.1	GI:38426732		
VERSION	AY373823				
KEYWORDS	AY373823				
SOURCE	AY373823	Saprolignia diclina			
ORGANISM	AY373823	Saprolignia diclina			
REFERENCE	AY373823	Eukaryota; stramenopiles; Oomycetes; Saproligniales;			
AUTHORS	AY373823	Saproligniaceae; Saprolignia.			
TITLE	AY373823	1 (bases 1 to 1077)			
JOURNAL	AY373823	Pereira, S.L., Huang, Y.S., Bobik, E.G., Kinney, A.J., Stecca, K.L.,			
PUBLISHED	AY373823	Packer, J.C. and Mukerji, P.			
AUTHORS	AY373823	A novel omega3-fatty acid desaturase involved in the biosynthesis			
TITLE	AY373823	of eicosapentaenoic acid			
JOURNAL	AY373823	Biochem. J. 378 (Pt 2), 665-671 (2004)			
PUBLISHED	AY373823	14651475			
REFERENCE	AY373823	2 (bases 1 to 1077)			
AUTHORS	AY373823	Pereira, S.L., Mukerji, P. and Huang, Y.-S.			
TITLE	AY373823	Direct Submission			
JOURNAL	AY373823	Submitted (25-AUG-2003) 104060, Abbott Laboratories-Ross Products			
FEATURES	AY373823	Division, RP4-3, 3300 Stelzer Road, Columbus, OH 43219, USA			
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ORIGIN
Alignment Scores:
Pred. No.: 5,12e-183 Length: 1077
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 8 Gaps: 0

US-10-060-793A-26 (1-358) x AY373823 (1-1077)
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DB 1 ATGACTGAGGATGAGCAAGGTCGAGTTCGCCAGCTCAGGAGCTCAAGCACTCGATC 60
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QY 101 SerValAsnPheIleIleGlyCysIleMetHisSerAlaIleLeuThrProPheGluSer 120
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QY 121 TrpArgValThrHisArgHisHisHisLysAsnThrGlyAsnIleAspLysAspGluIle 140
DB 361 TGGCGGTGACGACCCGCCACCAACCAAGAACACGGGCAACATTGNTAAGGACGAGATC 420
QY 141 PheTyrProHisArgSerValLysAspLeuGlnAspValArgGlnTrpValTyrThrLeu 160
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QY 181 AspProTrpAspProLeuLeuLeuLeuArgAlaSerAlaValIleValSerLeuGlyVal 200
DB 541 GACCCGTGGAGCCCGCTCTCTTCTCGCGCGCGCTCGGCCGCTCATGCTGCTCGGCGTC 600
QY 201 TrpAlaAlaPhePheAlaAlaTyrAlaTyrLeuThrTyrSerLeuGlyPheAlaValMet 220

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Db 601 TGGGCGCGCTTCTTCGCGCGGTACGGGTACCTCACATACTCGCTCGCTTTCGCGTCATG 660
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DB 661 GGCTCTACTACTATGCGCGCTCTTTGCTTTTGGTTTGGTTTCTGCTTATTAGACCTTC 720
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QY 261 GlyAsnLeuSerSerValAspArgSerTyrGlyAlaPheValAspAsnLeuSerHisHis 280
DB 781 GGCAACCTCTCGAGCGTCGACCGCTCGTACGGCGCTTCGTGGACAACTGAGCCACAC 840
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QY 321 IleThrAlaPhePheLysThrAlaHisLeuPheValAsnTyrGlyAlaValProGluThr 340
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ACCESSION AP003586.1 GI:17135283
VERSION
KEYWORDS
SOURCE Nostoc sp. PCC 7120
ORGANISM Nostoc sp. PCC 7120
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
REFERENCE
AUTHORS Kaneko,T., Nakamura,Y., Wolk,C.P., Kuritz,T., Sasamoto,S.,
Watanabe,A., Iriguchi,M., Ishikawa,A., Kawashima,K., Kimura,T.,
Kishida,Y., Kohara,M., Matsumoto,M., Matsuno,A., Muraki,A.,
Nakazaki,N., Shimpo,S., Sugimoto,M., Takazawa,M., Yamada,M.,
Yasuda,M. and Tabata,S.
Complete genomic sequence of the filamentous nitrogen-fixing
cyanobacterium Anabaena sp. strain PCC 7120
DNA Res. 8 (5), 205-213 (2001)
JOURNAL MEDLINE 21595285
PUBMED 11759840
REFERENCE 2 (bases 1 to 349050)
AUTHORS Kaneko,T.
DIRECT SUBMISSION
TITLE Submitted (02-MAY-2001) Takakazu Kaneko, Kazusa DNA Research
Institute, The First Laboratory for Plant Gene Research; Yana
1532-3, Kisarazu, Chiba 292-0812, Japan
JOURNAL (E-mail:kaneko@kazusa.or.jp,
URL:http://www.kazusa.or.jp/cyanobase/,
Tel:81-438-52-3935(ex.2338), Fax:81-438-52-3934)
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 11, 2005, 06:12:47 ; Search time 4032 Seconds  
(without alignments)  
3379.714 Million cell updates/sec

Title: US-10-060-793A-26

Perfect score: 1929

Sequence: 1 MTEDKTKVEPPTLTTELKHSI.....ETRAQIFTLKESAAAAAKAKSD 358

Scoring table:

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
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Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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4: gb\_est3.\*  
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6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_ges1.\*  
9: gb\_ges2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	824	42.7	664	7	CF840561 psHB009xD
2	647	33.5	643	2	BE777235 MY-26-A-1
3	595	30.8	597	7	CF850773 pMA015xP
4	574.5	29.8	683	2	BE776116 MY-11-B-0
5	529	27.4	1520	3	AY107103 Zea mays
6	526	27.3	1636	3	AY111307 Zea mays
7	503.5	26.1	1365	3	CNS0484L Arabidops
8	499	25.9	1516	3	CNS092RR Arabidops
9	492.5	25.5	1554	3	CNS044NN Arabidops

10	484.5	25.1	1513	3	CNS0A5G7
11	484.5	25.1	1528	3	CNS0A5PZ
12	482.5	25.0	1513	3	CNS0A5LO
13	469.5	24.3	831	7	CF215869
14	465	24.1	1856	3	AY104050
15	460.5	23.9	833	7	CO097259
16	460	23.8	869	8	CC32198
17	458.5	23.8	790	7	CF443330
18	458	23.7	1807	4	B1683572
19	454	23.5	737	5	BQ874237
20	453	23.5	826	9	CG438073
21	451	23.4	900	9	CG442730
22	450	23.3	724	5	BQ871133
23	448.5	23.3	732	1	AJ795089
24	441.5	22.9	757	7	CN144925
25	440	22.8	727	5	BU009141
26	437	22.7	975	9	CG304699
27	436.5	22.6	707	6	CD882139
28	435	22.6	776	9	CL187144
29	432	22.4	840	7	COL13447
30	427.5	22.2	863	7	CO082075
31	426.5	22.1	827	7	CO094468
32	422.5	21.9	824	7	CV290982
33	420	21.8	661	5	BU041344
34	418	21.7	1084	7	CK210592
35	417.5	21.6	868	7	COL19917
36	417	21.6	771	9	CC731290
37	414.5	21.5	763	5	BQ853589
38	409.5	21.2	703	5	BQ625067
39	408	21.2	701	5	BQ876051
40	407	21.1	924	8	CC338891
41	407	21.1	1065	9	CL981518
42	405.5	21.0	809	2	BE998745
43	405.5	21.0	989	7	CK269848
44	405	21.0	664	5	BQ767472
45	400	20.7	811	7	CF444900

#### ALIGNMENTS

RESULT 1

LOCUS

DEFINITION

CF840561 664 bp mRNA linear EST 30-OCT-2003  
psHB009XD12f USDA-IFAFS:Expression of Phytophthora sojae genes  
during infection and propagation\_SHB Phytophthora sojae cDNA clone  
SHB009D12 5, mRNA sequence.

ACCESSION

CF840561 GI:38056215

VERSION

EST.

KEYWORDS

SOURCE

Phytophthora sojae

Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;

Phytophthora.

1 (bases 1 to 664)

Tyler, B.

Tyler, B. Not Published

Unpublished (2003)

Contact: Tyler B

Tyler lab

VBI

1880 Pratt Dr., Blacksburg, VA 24061, USA

Tel: 540-231-7318

Email: bmttyler@vt.edu

PCR Primers

FORWARD: BK reverse primer

BACKWARD: BK reverse primer

Plate: 009 row: D column: 12

Seq primer: BK reverse primer

High quality sequence stop: 664.

Location/Qualifiers

1..664

/organism="Phytophthora sojae"

/mol\_type="mRNA"

FEATURES

source



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 11, 2005, 06:12:41 ; Search time 671 Seconds

(without alignments)

3158.372 Million cell updates/sec

Title: US-10-060-793a-26

Perfect score: 1929

Sequence: 1 MTEDKTKVERPFLTELKHSI.....ETRAQIFLKESAAAKAKSD 358

Scoring table: BLOSUM62

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1929	100.0	1077	10 AAD58792	Aad58792 Saprolegn
2	1929	100.0	1077	13 ADR20168	Adr20168 Saprolegn
3	586.5	30.4	1080	13 ADS48002	Ads48002 Bacterial
4	586.5	30.4	2001	12 ADM47683	Adm47683 Polynucle
5	582	30.2	999	13 ADT44325	Adt44325 Bacterial

6	572.5	29.7	1041	13 ADT45348	Adt45348 Bacterial
7	538.5	27.9	2090	4 AAH5810	Aah5810 Chlorella
8	523.5	27.1	1242	10 AAD57627	Aad57627 Rice abio
9	520.5	27.1	1405	12 ADJ81721	Adj81721 Mutant so
10	520.5	27.0	1675	2 AAQ43208	Aaq43208 Sequence
11	516.5	26.8	1543	12 ADO44397	Ado44397 Z. mays F
12	516.5	26.8	1900	12 ADM47680	Adm47680 Polynucle
13	514	26.6	1245	8 ADA71116	Ada71116 Rice gene
14	512	26.5	1279	10 ADK58843	Adk58843 Plant DNA
15	510	26.4	1308	6 ABZ12830	Abz12830 Arabidops
16	510	26.4	1308	8 ADA68613	Ada68613 Arabidops
17	510	26.4	1525	2 AAQ71211	Aaq71211 Linoleic-
18	510	26.4	1525	12 ADM47682	Adm47682 Polynucle
19	510	26.4	1525	13 ADS12589	Ads12589 Arabidops
20	506.5	26.3	1376	12 ADJ81722	Adj81722 Mutant so
21	506.5	26.3	1395	12 ADJ81723	Adj81723 Mutant so
22	505.5	26.2	1353	2 AAQ71203	Aaq71203 Linoleic-
23	505	26.2	2181	2 AAQ43207	Aaq43207 Sequence
24	503.5	26.1	1161	12 ADM73744	Adm73744 Thale cre
25	503.5	26.1	1268	3 AAC44312	Aac44312 Arabidops
26	503.5	26.1	1350	2 AAQ43202	Aaq43202 Sequence
27	503.5	26.1	1350	13 ADR20174	Adr20174 Arabidops
28	503.5	26.1	1350	13 ADS12587	Ads12587 Arabidops
29	503	26.1	1475	9 AAD54575	Aad54575 Flax omeg
30	500.5	25.9	1429	2 AAQ43205	Aaq43205 Sequence
31	500.5	25.9	1429	2 AAQ43206	Aaq43206 Sequence
32	499.5	25.9	1525	2 AAQ43204	Aaq43204 Sequence
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34	499.5	25.9	1662	12 ADM47681	Adm47681 Polynucle
35	499.5	25.9	1662	13 ADS12585	Ads12585 Arabidops
36	499	25.9	1549	4 AAC82092	Aac82092 E. guinee
37	497	25.8	1142	4 AAC02364	Aac02364 Braesica
38	493.5	25.6	1429	3 AAC33624	Aac33624 Arabidops
39	492	25.5	1152	13 ADR87344	Adr87344 DeltakKGG
40	492	25.5	1164	10 ABZ58386	Abz58386 Caenor be
41	492	25.5	1164	13 ADR87347	Adr87347 Codon opt
42	492	25.5	1164	13 ADR87320	Adr87320 Hydroxyla
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44	492	25.5	1216	4 AAC89457	Aac89457 DNA found
45	489.5	25.4	1621	2 AAT62066	Aat62066 Sesame om

#### ALIGNMENTS

RESULT 1  
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ID AAD58792 standard; DNA; 1077 BP.  
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AC AAD58792;  
XX  
DT 04-DEC-2003 (first entry)  
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DE Saprolegina diclina omega-3 desaturase gene.  
XX  
KW Polyunsaturated fatty acid; PUFA; omega-3 desaturase; AIDS; cosmetic;  
KW delta-12 desaturase; acquired immune deficiency syndrome; gene therapy;  
KW inflammatory skin disorder; delta-17 desaturase; eczema; animal feed;  
KW multiple sclerosis; enzyme; gene; ds.  
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OS Saprolegina diclina.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1077  
FT /tag= a  
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XX WO2003064596-A2.  
XX  
PD 07-AUG-2003.  
XX  
PF 21-JAN-2003; 2003WO-US001698.  
XX  
PR 30-JAN-2002; 2002US-00060793.

XX (ABBO ) ABBOTT LAB.  
 XX Mukerji P, Pereira SL, Huang Y;  
 XX WPI; 2003-689526/65.  
 DR P-PSDB; AAE38732.  
 XX New isolated nucleic acid sequence encoding a polypeptide having  
 PT desaturase activity, useful for preventing or treating eczema,  
 PT burned or dry skin, AIDS, multiple sclerosis, or inflammatory skin  
 PT disorders.  
 XX Claim 2; Fig 9B; 137pp; English.  
 XX The invention is directed to the identification and isolation of novel  
 CC genes that encode enzymes involved in the synthesis of polyunsaturated  
 CC fatty acids (PUFAs). In particular the invention is directed to genes  
 CC derived from the fungus *Saprolegnia diclina* that encode omega-3  
 CC desaturase (also referred to as delta-17 desaturase) and delta-12  
 CC desaturase. Polynucleotides, composition and methods of the invention are  
 CC useful for preventing or treating conditions caused by insufficient  
 CC intake of at least one PUFA e.g. eczema, burned or dry skin, acquired  
 CC immune deficiency syndrome (AIDS), multiple sclerosis or inflammatory  
 CC skin disorders. Products produced in the method of the invention are  
 CC useful in pharmaceutical and nutritional compositions, animal feeds and  
 CC cosmetics. The invention is also useful in gene therapy. The present  
 CC sequence is *Saprolegnia diclina* omega-3 desaturase gene  
 XX  
 SQ Sequence 1077 BP; 191 A; 379 C; 286 G; 221 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 2,48e-219 Length: 1077  
 Score: 1929.00 Matches: 358  
 Percent Similarity: 100.00% Conservative: 0  
 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 10 Gaps: 0

US-10-060-793A-26 (1-358) x AAD58792 (1-1077)

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 Qy 21 ProAsnAlaCysPheGluSerAsnLeuGlyLeuSerLeuTyrThrAlaArgAlaIle 40  
 Db 61 CCGAACCGGCTTGTAGTGAACCTCGGCTCTCTACTACACGGCCCGCGGATC 120  
 Qy 41 PheAsnAlaSerAlaSerAlaLeuLeuTyrAlaAlaArgSerThrProPheIleAla 60  
 Db 121 TTCACGCGTCGGCTCGGGGGCTGCTCTACGGGGGGCTCGAGCGCTTCATGTCC 180  
 Qy 61 AspAsnValLeuLeuHisAlaLeuValCysAlaThrTyrIleTyrValGlnGlyValIle 80  
 Db 181 GATAACGCTTCTGCTCCACGGCTGCTTGGCCACCTACATCTACGTGACGGGCGTCATC 240  
 Qy 81 PheTrpGlyPheThrValGlyHisAspCysGlyHisSerAlaPheSerArgTyrHis 100  
 Db 241 TTCGGGGCTTCTTCACGGTCGGCGACGACTGCGGCACCTCGGCTCTCTCGCTACCC 300  
 Qy 101 SerValAsnPheIleIleGlyCysIleMetHisSerAlaIleLeuThrProPheGluSer 120  
 Db 301 AGCGTCACTTATCATCGCTGCATCATGCACTCTGCGATTCTTTCAGCGCTTCGAGAGC 360  
 Qy 121 TrpArgValThrHisArgHisHisLysAsnThrGlyAsnIleAspLysAspGluIle 140  
 Db 361 TGGCGGTGACGACCGCCACCAACCAAGAACCGGGCAACATTGATAAGGACGAGATC 420  
 Qy 141 PheTyrProHisArgSerValLysAspLeuGlnAspValArgGlnTrpValTyrThrLeu 160  
 Db 421 TTTTACCCGACCGGTCGGTCAAGGACCTTCAGGACGTGCGCAATGGGTCTACAGCTC 480

Qy 161 GlyGlyAlaTrpPheValTyrLeuLysValGlyTyrAlaProArgThrMetSerHisPhe 180  
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 Db 541 GACCCGTGGGACCCGCTCCTCTTCGCGCGCTCGCGCTCATCGTGTGCTCGGCGTC 600  
 Qy 201 TrpAlaAlaPhePheAlaAlaTyrAlaTyrLeuThrTyrSerLeuGlyPheAlaValMet 220  
 Db 601 TGGCGCGCTTCTTCGCGCGTACGGTACCTCACATACCTCGCTCGCTTTCGCGCATG 660  
 Qy 221 GlyLeuTyrTyrTyrAlaProLeuPheValPheAlaSerPheLeuValIleThrPhe 240  
 Db 661 GGCTCTACTACTATGCGCGCTCTTTGTCTTGTCTTCGTTCTCGTCAATACGACCTTC 720  
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 Qy 261 GlyAsnLeuSerSerValAspArgSerTyrGlyAlaPheValAspAsnLeuSerHisHis 280  
 Db 781 GGCAACCTCTCGAGCTGACCTCGTACGGCGCTTCGTGGACAACCTGAGCCACCAC 840  
 Qy 281 IleGlyThrHisGlnValHisLeuPheProIleIleProHisTyrLysLeuAsnGlu 300  
 Db 841 ATTGGCAGCAGCAGCTCCACCACTTGTTCGATCATTCGACCTACAAGCTCAAGAA 900  
 Qy 301 AlaThrLysHisPheAlaAlaTyrProHisLeuValArgAsnAspGluProIle 320  
 Db 901 GCCACCAAGCACTTTCGCGCGCTACCGGCTCGTGGCAGGAACGACGAGCCCATC 960  
 Qy 321 IleThrAlaPhePheLysThrAlaHisLeuPheValAsnTyrGlyAlaValProGluThr 340  
 Db 961 ATCAGCGCTTCTTCAAGACCGCGCACCTCTTTGTCACTACGCGCTGTGCCCCGAGACG 1020  
 Qy 341 AlaGlnIlePheThrLeuLysGluSerAlaAlaAlaAlaLysAlaLysSerAsp 358  
 Db 1021 GCGCAGATCTTCACGCTCAAGAGTTCGGCGCGCCGCCCAAGTCCGAC 1074  
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 ID ADR20168 standard; cDNA; 1077 BP.  
 XX  
 AC ADR20168;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE Saprolegnia diclina delta-17 desaturase encoding cDNA SEQ ID NO:41.  
 XX  
 KW oilseed plant; mature seed; seed fatty acid profile;  
 KW polyunsaturated fatty acid; delta-17 desaturase; oil; food; food product;  
 KW beverage; infant formula; nutritional supplement; pet food; animal feed;  
 KW whole bean soy product; aquaculture food product; enzyme; gene; ss.  
 XX  
 OS Saprolegnia diclina.  
 XX  
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 FT /product= "delta-17 desaturase"  
 XX  
 XX WO2004071467-A2.  
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 XX 26-AUG-2004.  
 XX  
 XX 12-FEB-2004; 2004WO-US005758.  
 XX  
 XX 12-FEB-2003; 2003US-0446941P.  
 PR  
 XX (DUPO ) DU PONT DE NEMOURS & CO E I.  
 PA  
 XX Kinney AJ, Cahoon EB, Damude HG, Hitz WD, Kolar CW, Liu Z;  
 PI

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: October 11, 2005, 06:12:47 ; Search time 221 Seconds  
(without alignments)

2650.620 Million cell updates/sec

Title: US-10-060-793A-26

Perfect score: 1929

Sequence: 1 MTEDKTKVEPPTLTKLHSI.....ETQIFTLKESAAAKAKSD 358

Scoring table:

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Ygapop 10.0 , Ygapext 0.5  
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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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5	510	26.4	1525	5	PCT-US94-01321-11
6	508.5	26.4	1353	5	US-09-330-235-7
7	508.5	26.4	1353	5	PCT-US94-01321-1
8	503.5	26.1	1350	2	US-08-244-205-1
9	503.5	26.1	1350	5	PCT-US92-10284-1
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11	500.5	25.9	1429	5	US-08-244-205-8
12	500.5	25.9	1429	5	PCT-US92-10284-6

13	500.5	25.9	1429	5	PCT-US92-10284-8	Sequence 8, Appl
14	499.5	25.9	1525	2	US-08-244-205-4	Sequence 4, Appl
15	499.5	25.9	1525	5	PCT-US92-10284-4	Sequence 4, Appl
16	499.5	25.9	1645	5	PCT-US94-01321-9	Sequence 9, Appl
17	492	25.5	1222	1	US-08-314-596-43	Sequence 43, Appl
18	492	25.5	1222	1	US-08-320-982-43	Sequence 43, Appl
19	492	25.5	1222	3	US-08-819-037-43	Sequence 43, Appl
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21	492	25.5	1448	1	US-08-314-596-39	Sequence 39, Appl
22	492	25.5	1448	1	US-08-320-982-39	Sequence 39, Appl
23	492	25.5	1448	3	US-08-819-037-39	Sequence 39, Appl
24	492	25.5	1448	3	US-09-045-940-39	Sequence 39, Appl
25	481.5	25.0	1369	3	US-09-133-962A-11	Sequence 11, Appl
26	465	24.1	1790	3	US-09-133-962A-7	Sequence 7, Appl
27	459.5	23.8	1462	3	US-09-133-962A-5	Sequence 5, Appl
28	458	23.7	1155	3	US-08-907-608-5	Sequence 5, Appl
29	458	23.7	1155	3	US-09-354-231B-5	Sequence 5, Appl
30	458	23.7	1155	3	US-09-354-231B-7	Sequence 7, Appl
31	458	23.7	1155	3	US-09-128-602B-5	Sequence 5, Appl
32	458	23.7	1155	3	US-09-128-602B-7	Sequence 7, Appl
33	458	23.7	1155	3	US-09-482-287-5	Sequence 5, Appl
34	458	23.7	1155	4	US-09-966-888-5	Sequence 5, Appl
35	458	23.7	1155	4	US-09-995-297-5	Sequence 5, Appl
36	458	23.7	1155	4	US-09-995-297-7	Sequence 7, Appl
37	457	23.7	1155	3	US-09-354-231B-9	Sequence 9, Appl
38	457	23.7	1155	3	US-09-128-602B-9	Sequence 9, Appl
39	457	23.7	1155	4	US-09-995-297-9	Sequence 9, Appl
40	457	23.7	1426	3	US-09-133-962A-3	Sequence 3, Appl
41	455	23.6	1155	3	US-08-907-608-3	Sequence 3, Appl
42	455	23.6	1155	3	US-09-482-287-3	Sequence 3, Appl
43	455	23.6	1155	4	US-09-966-888-3	Sequence 3, Appl
44	454	23.5	1155	3	US-09-354-231B-11	Sequence 11, Appl
45	454	23.5	1155	3	US-09-128-602B-11	Sequence 11, Appl

#### ALIGNMENTS

#### RESULT 1

US-08-244-205-10  
; Sequence 10, Application US/08244205  
; Patent No. 5952544  
; GENERAL INFORMATION:  
; APPLICANT: Browse, John, Kinney, Anthony J.,  
; APPLICANT: Pierce, John, Wierzbicki, Anna M.,  
; APPLICANT: Yadav, Narendra S., Perez-Grau, Luis  
; TITLE OF INVENTION: Fatty Acid Desaturase Genes  
; TITLE OF INVENTION: from Plants  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: E. I. du Pont de Nemours and Company  
; STREET: 1007 Market Street  
; CITY: Wilmington  
; STATE: Delaware  
; COUNTRY: U.S.A.  
; ZIP: 19898  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Macintosh  
; OPERATING SYSTEM: Macintosh System, 6.0  
; SOFTWARE: Microsoft Word, 4.0  
; CURRENT APPLICATION NUMBER: US/08/244,205  
; APPLICATION NUMBER: 07/804,259  
; FILING DATE: 4 DECEMBER 1991  
; CLASSIFICATION: 800  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/804,259  
; FILING DATE: 4 DECEMBER 1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Floyd, Linda A.  
; REGISTRATION NUMBER: 33,692  
; REFERENCE/DOCKET NUMBER: BB-1036-A  
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